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Nucleic Acids, Proteins, and Artibodies

Statement under 37 C.F.R. § 1.77(b)(4)

This application refers to a "Sequence Listing' listed below, which is provided as an electronic document on two identical compact discs (CD-R), labeled "Copy 1" and "Copy 2." These compact discs each contain the following files, which are hereby incorporated in their entirety herein:

Document	File Name	Size in bytes	Date of Creation
Sequence Listing	PTZ32_seqList.txt	3,411,250	01/15/2001
V Viewer Setup File	SetupDLL.exe	695,808	12/19/2000
V Viewer Help File Controller	v.cnt	7,984	01/05/2001
V Viewer Program File	v.exe	753,664	12/19/2000
V Viewer Help File	v.hlp	447,766	01/05/2001

[2] The Sequence Listing may be viewed on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, licensed by HGS, Inc., included on the compact discs (see World Wide Web URL: http://www.fileviewer.com).

Field of the Invention

The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic

methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

- One of the most critical tasks a cell must perform is to respond to cues from its environment, i.e., extracellular signals. Some of the most important extracellular signals come from other cells. The ability for cells to be able to send and receive signals from one another is of paramount importance in multicellular organisms because it allows individual cells within a body to become highly specialized and yet work in a coordinated fashion with other cells of the body. Cellular signaling mechanisms regulate a variety of cellular processes such as, for example, proliferation, differentiation, survival, movement, and secretion. Defects in cellular signaling can lead to a number of diseases and disorders such as cancers, immune system disorders and nervous system disorders. For more expansive reviews on this subject, please refer to Hunter, *Cell* 100:113-127 and Chapter 15 of *Molecular Biology of the Cell*, Third Edition, edited by Alberts et al. (1994), which are herein incorporated by reference in their entirety.
- Signal transduction requires molecules that serve as the extracellular signaling molecules as well as a set of receptors that "receive" the signal. Frequently, an additional set of proteins is necessary in order for the cell to translate the signal it has received into an appropriate response via the activation or inhibition of a particular set of genes or proteins. The signaling molecules, the receptor proteins, and the molecules that relay the signal between the receptor and the final effector molecules collectively form what are known as signal transduction pathways.
- To date, several common types of signal transduction pathways have been identified. One way to classify a signal transduction pathway is based on the class of receptor protein it utilizes. Two well known classes of receptor proteins are G-protein coupled receptors and enzyme-linked receptors. This latter class of enzyme-linked receptors includes receptor tyrosine kinases, tyrosine kinase associated receptors, receptor serine/threonine kinases, receptor tyrosine phosphatases, and receptor guanylyl cyclases.

Signal Transduction through G-protein Coupled Receptors

G protein coupled receptors are the largest family of cell surface receptors. They are seven-pass transmembrane receptors which activate trimeric G proteins (G proteins) upon ligand binding. G proteins are GTPases composed of three subunits: alpha, beta and gamma. G proteins function as molecular switches existing in two states: an active GTP bound state and an inactive GDP bound state. Ligand binding to G protein coupled receptors induce inactive G proteins to release GDP allowing GTP to bind in its place. Binding of GTP to a G protein causes the alpha subunit to dissociate from the beta and gamma subunits which remain associated with one another. Eventually, the GTPase activity of the alpha subunit results in hydrolysis of the bound GTP molecule to GDP, thus inactivating the G protein.

There are several types of G proteins that have been classified based upon their function. Stimulatory G proteins (G_s) are involved in adenylate cyclase activation; inhibitory G proteins (G_i) function to inhibit the activity of adenylate cyclase. Yet another type of G protein , G_q proteins, functions in the activation of phosphoinositide-specific phospholipase C enzyme.

[9] Activation of adenylate cyclase by an activated G_s protein results in the production of the cyclic nucleotide, cyclic AMP (cAMP). cAMP mediates its effects mostly through its activation of cAMP dependent kinase (A-kinase), a serine/threonine kinase. Activation of A-kinase helps to further relay the signal from the G protein coupled receptor to the target proteins. In muscle cells, for instance, activation of A-kinase following adrenaline signaling ultimately results in the activation of an enzyme, glycogen phosphorylase, which catalyzes the release of glucose molecules which can be used to produce energy from glycogen. In other instances, activated A-kinase translocates to the nucleus where it phosphorylates the cAMP response element binding (CREB) protein, which when phosphorylated, acts as a transcription factor to stimulate the expression of genes that have cAMP response elements (CRE) sequences in their regulatory regions.

[10] G_q proteins, when activated, activate the enzyme phospholipase C-beta which hydrolyzes PI 4,5-biphosphate (PIP₂) producing inositol triphosphate (IP₃) and diacylglycerol (DAG). IP₃ functions as a second messenger that causes the release of Ca²⁺ from intracellular stores. Released calcium then binds to Ca²⁺ binding proteins such as calmodulin, which in its calcium bound state, is able to activate Ca²⁺/calmodulin dependent protein kinases (CaM-kinases). Activated CaM kinases then continue to relay the signal to

more downstream molecules in the signal transduction pathway. The other product produced by phospholipase C-beta, DAG, functions to activate the serine/threonine kinase known as protein kinase C (PKC). Activated PKC phosphorylates target proteins depending on the cell type, and in many cells these phosphorylation events lead to the increased transcription of specific genes. The highest concentrations of protein kinase C are found in the brain where PKC phosphorylates ion channels in nerve cells thereby altering their excitability. PKC activation can be induced by treating cells with phorbol esters which are able to cross the plasma membrane, bind to, and activate PKC directly.

Signal Transduction through Receptor Tyrosine Kinases

- [11] The receptor protein tyrosine kinases (RPTKs) are some of the most well studied receptors, and the signaling cascades they initiate demonstrate two of the fundamental concepts in signal transduction: the regulation of protein phosphorylation and the recruitment of proteins into a signaling cascade via protein-protein interaction domains.
- [12] Binding of the cognate ligand to a RPTK, such as epidermal growth factor (EGF) binding to the epidermal growth factor receptor (EGFR), induces RPTKs to dimerize and cross-phosphorylate each other on multiple tyrosine residues. The phosphorylated receptor dimer is the activated form of the receptor.
- [13] The phosphorylated tyrosines on activated RPTKs are then recognized/bound by other components of the signal transduction pathway. One of the important discoveries in the field of signal transduction was the recognition of conserved domains which allow for protein-protein interactions in signaling pathways. The most prevalent binding domain that recognizes phosphotyrosine (P-Tyr) residues is known as the SH2 domain (for Src homology region 2, named after the Src protein in which the SH2 domain was first discovered). Another domain that recognizes P-Tyr residues is called the P-Tyr binding domain (PTB). The discovery of the SH2 domain was quickly followed by the discovery of several other protein-protein interaction domains involved in signal transduction and by the realization that most of these domains are modular in nature, meaning these domains fold independently - a most convenient feature for protein engineering. To date, more than 100 such protein interaction domains involved in signaling have been defined via comparative sequence analysis. Most of these domains recognize short linear sequences (approximately 4-10 amino acid residues in length), in some cases requiring phosphorylation of specific residues within the sequence allowing for inducible association. A convenient web based database, with

links to abstracts of papers characterizing these domains can be found at http://smart.EMBL-Heidelberg.de.

Proteins containing SH2 and PTB domains translocate to the plasma membrane [14] where they associate with the activated RPTKs which, in turn, activates them through phosphorylation. By way of example, activation of the platelet derived growth factor receptor (PDGFR) results in the autophosphorylation of tyrosine residues in the cytoplasmic tail of the PDGFR. These P-Tyr residues then serve as the binding sites for other proteins, such as a GTPase (discussed in more detail below), phospholipase C-gamma, and the regulatory subunit of PI-3-kinase, which are each able to recognize the P-Tyr residues in PDGFR via SH2 domains. The interaction of these proteins with the activated PDGFR results in the translocation of these proteins to the plasma membranes where they have their substrates and the PDGFR mediated activation of these proteins via phosphorylation.

In the previous example, each of the proteins recruited to the activated RPTK via [15] their SH2 domains also had catalytic activities that allowed them to propagate a signal. There are proteins involved in signal transduction, however, which have no ability in and of themselves to propagate a signal. Instead, these proteins, known as adaptor proteins, serve -to couple activated RPTKs to other components of the signal transduction pathway which do have the capacity to propagate the signal. One such adaptor protein is known as Grb2. It contains one SH2 domain and two SH3 domains (another Src homology domain that mediates protein interactions). Grb 2 is constitutively associated with Sos protein, a guanine nucleotide releasing protein (GNRP), via its SH3 domain. Thus, when Grb2 associates with an activated receptor via its SH2 domain, it also brings Sos into proximity with the RPTK which activates the Sos protein via phosphorylation.

[16] GNRP proteins, such as Sos, are one of two types of proteins that help regulate the activity of proteins belonging to the Ras superfamily of monomeric GTPases. Ras proteins are proteins that are associated with the cytoplasmic side of the plasma membrane and help relay signals from RPTK to the nucleus to stimulate cell proliferation or differentiation. Ras proteins exist in two states, an inactive state in which ras is bound to GDP and an active state in which ras is bound to GTP. Activated GNRP proteins promote the exchange of bound GDP for GTP on ras proteins, thereby activating ras. Ras, itself, is a GTPase that hydrolyzes GTP to GDP, and would therefore tend to inactivate itself over time. However, ras is an inefficient GTPase, so the inactivation of ras is enhanced by GTPase activating proteins (GAPs) which increase the rate of hydrolysis of GTP by ras.

[17] Activated Ras kinases then act to activate more downstream signaling events, including activation of the mitogen-activated protein kinase (MAPK) pathway which is a cascade of serine/threonine kinases. Ras binds to and activates a MAPK kinase kinase (MAPKKK, such as Raf-1, for example), which in turn activates a MAPK kinase (MAPKK) via phosphorylation, which in turn activates a MAPK. MAPKs relay signals downstream by phosphorylating various proteins in the cell including other kinases and/or regulatory proteins in the cell. For instance, an activated MAPK can enter the nucleus and help to initiate transcription of genes that must be expressed in order for the cell to respond to the extracellular signal, such as genes required for DNA replication in response to the extracellular proliferation signal.

[18] Another class of signaling receptors, receptor serine/threonine kinases (RSK) has recently been identified. An example of an RSK is the TGF-beta receptor. Additionally, it has also been recently recognized that there are modular binding domains that recognize phosphoserine/phosphothreonine (P-Ser/P-Thr) residues. For instance, 14-3-3 domains recognize phosphoserines in specific amino acid contexts [RSX(P-Ser)XP] or [R(Y/F)X(P-Ser)XP] and may function in the assembly of signaling complexes. Other residues such as histidine and arginine can also be phosphorylated, and it is possible that additional kinases which phosphorylate these residues, or protein domains that bind phosphohistidine or phosphoarginine will be discovered.

Signaling Via Intracellular Receptors

Some extracellular signals do not have cell surface receptors such as G protein coupled receptors or receptor tyrosine kinases. Instead, these extracellular signals are able to traverse the plasma membrane and interact with their receptors in the cytoplasm. Examples of such signals are the steroid hormones and the gas nitrous oxide (NO). The steroid hormone receptors, once bound by their ligand, are generally able to translocate to the nucleus where they bind regulatory DNA elements that control the gene expression of specific genes. NO gas, on the other hand, generally enters a cell and reacts with iron in the active site of the enzyme guanylate cyclase, stimulating it to produce cyclic GMP (cGMP). cGMP acts as a second messenger (similar to the way cAMP functions) and can stimulate further downstream signaling by binding to other proteins.

Terminating Signal Transduction

[20] As the effects of signal transduction are transient, there must also be mechanisms for terminating signal cascades. For example, G proteins are self-inactivating, and there are a set of proteins, GAPs, that are devoted to increasing the rate of hydrolysis of bound GTP by ras proteins. Cyclic nucleotide second messngers such as cAMP and cGMP are hydrolyzed by phosphodiesterases. In the case of kinases, there generally exist a set of complementary phosphatases that function to dephosphorylate phosphorylated residues, thereby bringing the signaling event to a close.

Signal Transduction Pathway Components and Disease

- Because signal transduction is involved in the regulation of so many cellular processes, including proliferation, differentiation, survival, and apoptosis, it is not surprising that defects in cellular signal transduction pathway components lead to a number of diseases and disorders, especially cancers. For a review on Signal transduction pathway components and diseases, see Hunter, Philosophical Transactions of the Royal Society of London Series B 353:583-605 (1998) which is herein incorporated by reference in its entirety. For instance, approximately 30% of human cancers have mutations in a ras gene, and at least 18 tyrosine kinases have been identified as oncogenes in either acutely transforming retroviruses or in human tumors, such as for example, Src. And more than 95% of chronic myelogenous leukemias express an activated form of the c-Abl non-receptor tyrosine kinases.
- [22] Mutations in signaling pathways are also implicated in a plethora of other diseases. Mutation in Bruton's tyrosine kinase leads to X-linked agammaglobulinemia. Inactivation of ZAP70 or JAK3 leads to a severe combined immunodeficiency disease. Coffin-Lowry syndrome occurs when the X-linked Rsk2 protein serine kinase gene is inactivated. Myotonic dystrophy occurs when expression of the myotonic dystrophy serine kinase gene is decreased. Overexpression of the aurora2 serine kinase is implicated in colon carcinoma.
- The malfunction of signal transduction pathway components, particularly kinases, in diseases indicate that these genes are good targets for drugs/pharmaceuticals that either inhibit or activate their function. In fact, some such drugs have been developed and are already in use or in clinical trials. For instance, an inhibitor of cyclin dependent kinase 2 (cdk2), a kinase important in regulating cellular proliferation, is in clinical trials for cancer treatment, as are inhibitors of epidermal growth factor receptor tyrosine kinases and vascular endothelial growth factor receptor (VEGFR) tyrosine kinases. Inhibition of VEGFR activity

reduces or eliminates the vascularization of tumors directed by VEGFR. An antagonistic monoclonal antibody, herceptin, against the erbB2 receptor tyrosine kinase is being used in breast cancer therapies to treat breast cancers where ErbB2 is overexpressed.

[24] Thus there exists a clear need for identifying and exploiting novel signal transduction pathway component polynucleotides and polypeptides. Although structurally related, such proteins may possess diverse and multifaceted functions in a variety of cell and tissue types. The inventive purified signal transduction pathway component polypeptides are research tools useful for the identification, characterization and purification of additional proteins involved in signal transduction. Furthermore, the identification of new signal transduction pathway component polynucleotides and polypeptides permits the development of a range of derivatives, agonists and antagonists at the nucleic acid and protein levels which in turn have applications in the treatment and diagnosis of a range of conditions such as, for example, cancer and other proliferative disorders (e.g., chronic myelogenous leukemia), immunological disorders (e.g., severe combined immunodeficiency and X-linked agammaglobulinemia), and nervous system disorders (Coffin-Lowry Syndrome), amongst other conditions.

Summary of the Invention

The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[26] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEO ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)". provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEO ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell

source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove nonspecific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIMTM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic

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sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

Table 2 summarizes homology and features of some of the polypeptides of the [28] invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[29] Table 3 provides polynucleotide sequences that may be disclaimed according to

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certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

- Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.
- [31] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM.

McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

- [32] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.
- [33] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.
- [34] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

- [35] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.
- In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.
- [37] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding

the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

In the present invention, "SEQ ID NO:X" was often generated by overlapping [38] sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[40] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS.

In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

- [42] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.
- [43] Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

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- [44] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.
- [45] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous

research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Freeman and Company, New York (1993); Η. Ed., T. Creighton, W. POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

- "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1Aor 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.
- [47] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an antipolypeptide antibody], immunogenicity (ability to generate antibody which binds to a

specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

- [48] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay signal transduction pathway component polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 38, 39, 49, 52-57, 64 and 67.
- [49] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).
- [50] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

TABLE 1A

Gene	Clone ID	Contig	Contig SEQ ID	ORF	AA	Predicted Epitopes	Tissue Distribution	Cytologic	OMIM
No:	NO: Z	: ::	NO: X	(From-To)	SEQ		Library code: count	Band	Disease
					<u>a</u>		(see Table IV for		Reference(s):
					NO: Y		Library Codes)		
_	HDPTE21	1165861		33 - 1790	624	Pro-16 to Gln-22,	AR051: 26, AR050:		
				•		Arg-34 to Asn-41,	22, AR054: 21, AR089:		
	-				,	Arg-49 to Lys-55,	1, AR061: 1		,
						Leu-156 to Thr-163,	H0529: 4, L0770: 4,		
						Glu-169 to Glu-174,	L0748: 4, L0749: 3,	-	
						Ser-198 to Glu-214,	L0777: 3, S0036: 2,		
						Glu-246 to Pro-252,	L0756: 2, S0360: 1,		-
						Arg-260 to Ser-271,	H0036: 1, H0318: 1,		
						Val-286 to Gly-291,	H0457: 1, H0051: 1,		
						Ser-304 to Glu-335,	H0328: 1, H0644: 1,		,
					,	Pro-436 to Pro-451,	S0002: 1, L0761: 1,		
		-) -				Ser-482 to Gly-487,	L0766: 1, L0804: 1,		
						Val-498 to Ser-505,	L0784: 1, H0521: 1 and		
						Asp-564 to Lys-585.	L0759: 1.	,	
		887711	443	1 - 639	1056				
		901381	444	570 - 112	1057	Gly-26 to Gly-32.			
2	H6EDR51	1197894	12	1 - 1935	625	Glu-35 to Gln-44,	AR089: 1, AR061: 1		
						Arg-70 to Val-77,	L0794: 11, L0777: 9,		

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H0255: 4, H0559: 4,	H0486: 3, H0581: 3,	L0809: 3, H0521: 3,	S0404: 3, H0556: 2,	H0580: 2, H0635: 2,	H0271: 2, H0135: 2,	H0703: 2, L0748: 2,	L0758: 2, H0543: 2,	H0422: 2, H0265: 1,	H0583: 1, H0656: 1,	H0638: 1, S0354: 1,	S0360: 1, H0637: 1,	Н0600: 1, Н0592: 1,	H0586: 1, H0587: 1,	H0257: 1, H0069: 1,	H0253: 1, S0049: 1,	H0199: 1, S0368: 1,	H0212: 1, H0494: 1,	H0529: 1, L0763: 1,	L0637: 1, L0761: 1,	L0630: 1, L0764: 1,	L0648: 1, L0768: 1,	L0766: 1, L0378: 1,	L0806: 1, L0655: 1,	L0657: 1, L0659: 1,	L0789: 1, H0593: 1,
Ala-113 to Gly-123,	Ser-128 to Phe-133,	Gly-235 to His-242,	Glu-249 to Leu-254,	Pro-286 to Arg-292,	Ser-309 to Glu-316,	Lys-337 to Glu-360,	Gln-366 to Gln-376,	Glu-383 to Ala-388,	Leú-391 to Leu-406,	Gln-413 to Ala-420,	Leu-430 to Leu-452,	Lys-461 to Glu-467,	Leu-476 to Lys-485,	Lys-491 to Arg-496,	Arg-500 to Gln-509,	Ala-513 to Asp-539,	Gln-544 to Ala-550,	Glu-569 to Val-576,	Arg-598 to Ser-620,	Asn-622 to Ala-627,	Ser-632 to Asn-645.				
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H0670: 1, S0378: 1, S0152: 1, H0696: 1, H0134: 1, L0779: 1, H0445: 1, H0542: 1 and			AR061: 3, AR089: 2	S0222: 1, H0575: 1,	H0618: 1, H0253: 1, H0266: 1, H0038: 1,	H0616: 1, L0643: 1,						
	Glu-26 to Gln-35, Arg-61 to Val-68, Ala-104 to Gly-114, Ser-119 to Phe-124, Gly-226 to His-233,	Glu-240 to Leu-245, Pro-277 to Arg-283.	Ser-5 to Arg-24,	1 rp-27 to Ala-52, Arg-48 to Gln-54,	Lys-71 to Gln-79, Pro-93 to His-101,	Lys-104 to Thr-110,	Val-141 to Pro-152,	Leu-158 to Gly-171,	Asn-183 to Ala-198, Gly-217 to Asp-233,	Ser-244 to Asn-258,	Lys-264 to Leu-269,	Ser-310 to Gly-316,
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								-	-	AR061: 1, AR089: 1	S0038: 1		AR061: 2, AR089: 1	L0439: 6, S0038: 3,	L0803: 3, H0455: 2,	L0769: 2, L0809: 2,	L0741: 2, L0756: 2,	S6024: 1, S0001: 1,	H0663: 1, S0222: 1,	H0441: 1, H0438: 1,	H0036: 1, S0049: 1,	H0309: 1, H0566: 1,	H0024: 1, S0388: 1,	S0051: 1, T0010: 1,	H0059: 1, L0645: 1,
Thr-326 to Glu-333,	Ser-396 to Pro-403,	Leu-416 to Lys-425.	Ser-3 to Arg-21,	Trp-24 to Ala-29,	Arg-45 to Gln-51,	Lys-68 to Gln-76,	Pro-90 to His-98,	Lys-101 to Thr-107,	Ser-116 to Gln-122.	Ser-6 to Pro-14.			Val-36 to Glu-43,	Lys-66 to Glu-71.											
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C0774: 1, L0790: 1,	L0663: 1, L0665: 1,	H0345: 1, L0742: 1,	.0748: 1, L0749: 1,	H0707: 1, L0595: 1 and	L0366: 1.	AR061: 1, AR089: 1	H0521: 14, L0439: 6,	.0754: 6, L0794: 4,	.0748: 4, S0278: 3,	.0766: 3, L0751: 3,	.0747: 3, L0749: 3,	H0556: 2, H0486: 2,	H0250: 2, H0179: 2,	H0271: 2, S0002: 2,	S0426: 2, L0770: 2,	L0769: 2, L0775: 2,	L0659: 2, L0411: 1,	S0134: 1, H0638: 1,	S0418: 1, S0420: 1,	50354: 1, S0358: 1,	S0360: 1, S0222: 1,	H0613: 1, H0052: 1,	H0051: 1, L0143: 1,	L0455: İ, H0124: 1,	H0090: 1, H0551: 1,
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	-					Pro-1 to Ser-10,	Pro-24 to Ser-29,	Pro-43 to Glu-61.		,															
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H0412: 1, S0038: 1, H0646: 1, S0344: 1, L0667: 1, L0772: 1, L0800: 1, L0662: 1, L0768: 1, L0804: 1, L0805: 1, L0790: 1, S0052: 1, H0593: 1,	H0518: 1, S0332: 1, S0027: 1, L0741: 1, L0743: 1, L0740: 1, L0779: 1, L0731: 1, L0758: 1, H0445: 1,	a 1	AR061: 5, AR089: 4 H0052: 2	AR089: 7, AR061: 3 H0521: 7, L0766: 5, H0318: 3, L0655: 3, H0522: 3, H0543: 3,
	-		His-1 to Cys-13, Glu-31 to Ala-49, Asp-82 to Pro-88. Glu-2 to Cys-11, Glu-29 to Ala-47, Asp-80 to Pro-86.	Asn-1 to Gly-6, Pro-34 to Arg-43, Lys-51 to Ile-56, Lys-58 to Arg-63,
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H0657: 2, H0553: 2,	L0632: 2, L0748: 2,	H0445: 2, L0605: 2,	H0422: 2, H0265: 1,	H0556: 1, S0114: 1,	H0583: 1, H0650: 1,	S0116: 1, H0341: 1,	S0360: 1, H0676: 1,	H0497: 1, H0486: 1,	H0075: 1, H0581: 1,	H0421: 1, S0388: 1,	H0271: 1, H0031: 1,	H0090: 1, H0591: 1,	H0038: 1, L0638: 1,	L0667: 1, L0363: 1,	L0774: 1, L0775: 1,	L0658: 1, L0659: 1,	L0809: 1, L0647: 1,	L0790: 1, H0701: 1,	H0658: 1, H0555: 1,	L0779: 1, L0777: 1,	L0731: 1 and H0423: 1.	AR054: 57, AR051:	36, AR050: 36, AR089:	4, AR061: 1	L0731: 19, L0766: 16,
Tyr-73 to Gly-85,	Ala-98 to Ala-104,	Ser-115 to Asp-124,	Gly-189 to Gly-194,	Pro-199 to Leu-204,	Ala-214 to Asp-225,	Thr-260 to Gln-268,	Pro-279 to Ser-284.						٠									Lys-13 to Gly-28,	Arg-64 to Gly-71,	Pro-131 to Glu-137,	Gln-152 to Asp-159,
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H0521: 11, L0748: 7,	L0754: 7, L0806: 6,	L0749: 6, L0794: 5,	L0666: 5, S0360: 4,	L0663: 4, L0740: 4,	L0747: 4, H0656: 3,	L0771: 3, L0662: 3,	L0774: 3, L0665: 3,	L0439: 3, L0777: 3,	L0755: 3, H0638: 2,	H0431: 2, H0620: 2,	H0494: 2, S0002: 2,	L0769: 2, L0803: 2,	L0438: 2, H0689: 2,	H0659: 2, H0658: 2,	H0518. 2, S0206: 2,	L0750: 2, S0242: 2,	H0423: 2, H0650: 1,	H0341: 1, H0661: 1,	H0662: 1, H0300: 1,	S0418: 1, S0376: 1,	H0580: 1, S0045: 1,	L0717: 1, H0453: 1,	H0370: 1, H0497: 1,	H0574: 1, H0632: 1,	H0486: 1, L0021: 1,
Lys-170 to Gly-179,	Thr-183 to Trp-188,	Arg-193 to Glu-206,	Asp-222 to Val-228,	Ser-262 to Ser-277.						•	,														,
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		-									,											Gln-1 to Gly-8,	Ile-15 to Asp-20,	Lys-61 to Glu-69,	Pro-93 to Lys-102,	Ala-147 to Leu-156,
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S0380: 2, H0423: 2,	H0624: 1, H0685: 1,	L0002: 1, H0583: 1,	L0760: 1, H0661: 1,	50358: 1, S0360: 1,	Н0637: 1, Н0601: 1,	H0486: 1, H0457: 1,	H0247: 1, S0003: 1,	T0067: 1, S0002: 1,	S0426: 1, H0529: 1,	L0770. 1, L0764: 1,	L0806: 1, L0655: 1,	L0659: 1, L0666: 1,	L0663: 1, L0664: 1,	S0428: 1, S0126: 1,	H0435: 1, H0521: 1,	H0522: 1, L0747: 1,	L0756: 1, L0759: 1,	H0445: 1 and H0422: 1.							
Pro-159 to Asp-174.													·						Ser-9 to Arg-14,	Arg-48 to Arg-54,	Gln-71 to Lys-77,	Ile-91 to Asp-96,	Lys-137 to Glu-145,	Pro-169 to Lys-178,	Ala-223 to Leu-232,
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		H0521: 9, L0595: 2,	L0593: 1 and L0594: 1.								AR051: 2, AR050: 1,	AR061: 1, AR054: 1,	AR089: 0	S0354: 8, H0254: 2,	S0358: 2, H0580: 2,	H0521: 2, H0656: 1,	H0590: 1, H0457: 1,	H0271: 1 and H0488: 1.			,			-		
	Pro-235 to Asp-250.	Asp-8 to Cys-21,	Val-25 to Asn-33,	Thr-47 to Pro-55,	Ala-62 to Thr-68,	Val-79 to Lys-88,	Asn-91 to Asn-104,	Tyr-114 to Gly-120,	Thr-187 to Glu-192,	Ile-217 to Thr-224.	Glu-94 to Tyr-102,	Pro-105 to Asn-112,	Thr-121 to Gly-137,	Glu-157 to Gly-162,	Glu-179 to Phe-186,	Cys-211 to Thr-222,	Ser-240 to Lys-245,	Thr-262 to Asn-279,	Arg-288 to Pro-306,	Asn-332 to Gln-339,	Ser-375 to Leu-382,	Arg-408 to Gly-415,	Asp-423 to Thr-428,	Ser-471 to Asn-476,	Pro-545 to Gly-551,	Ser-606 to Pro-616,
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								AR089: 2, AR061: 0	H0457: 9, L0596: 3,	L0803: 2, H0673: 1,	L0455: 1, L0369: 1,	L0764: 1, L0389: 1,	L0375: 1, L0655: 1,	L0809: 1, L0790: 1 and	L0752: 1.	AR061: 1, AR089: 1	H0009: 1	AR061: 4, AR089: 2	S0278: 4, H0581: 4,	L0751: 4, H0620: 3,	L0764: 3, L0662: 3,	L0659: 3, L0439: 3,	L0754: 3, H0542: 3,	H0170: 2, H0402: 2,]н0580: 2, Н0550: 2,
Ala-662 to Gly-667,	Thr-675 to Tyr-682,	Glu-714 to Trp-720,	Pro-722 to Val-732,	Pro-787 to Thr-795,	Arg-811 to Glu-816,	Gln-880 to Thr-891.		Ala-13 to Arg-20,	Gln-35 to Lys-48.	,								Arg-15 to Trp-20,	Asn-26 to Pro-34,	Lys-115 to Glu-125,	Glu-154 to Trp-163,	Ser-192 to Val-197,	Gly-216 to Arg-222.		
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H0333: 2, H0012: 2,	T0010: 2, H0252: 2,	H0063: 2, H0059: 2,	S0002: 2, L0775: 2,	L0655: 2, L0663: 2,	L0665: 2, H0593: 2,	H0658: 2, H0539: 2,	H0555: 2, L0743: 2,	L0744: 2, L0752: 2,	L0731; 2, H0543; 2,	H0624: 1, H0265: 1,	H0650: 1, H0656: 1,	S0212: 1, H0306: 1,	H0305: 1, S0360: 1,	S0046: 1, H0619: 1,	S0222: 1, S6014: 1,	H0613: 1, H0492: 1,	H0250: 1, H0635: 1,	H0427: 1, L0021: 1,	H0036: 1, H0421: 1,	H0399: 1, H0416: 1,	H0188: 1, S0250: 1,	L0143: 1, H0617: 1,	H0673: 1, H0124: 1,	H0163: 1, H0634: 1,	H0087: 1 T0067: 1
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											-		•		Arg-16 to Trp-21,	Asn-27 to Pro-35,	Lys-116 to Glu-126,	Glu-155 to Trp-164,	Ser-193 to Val-198,	Gly-217 to Arg-223.		·		Ser-1 to Ser-7,	Ser-25 to Arg-31.
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Lys-1 to Ala-6, Ser-38 to Gln-43.		•	Ser-19 to Thr-29,	Lys-62 to Arg-67,	Gln-102 to Phe-113.	Gly-1 to Ser-13,	Ile-24 to Phe-29.	Gly-9 to Gln-15.							. •						(
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					Gly-1 to Ile-11,	Pro-49 to Asp-59,	Val-64 to Leu-70,	Gly-105 to Ser-112,	Ser-130 to Ala-146,	Asn-223 to Val-229,	Asn-272 to Asp-278,	Lys-294 to Tyr-305.						Pro-46 to Asp-56,	Val-61 to Leu-67,	Gly-102 to Ser-109,	Ser-127 to Ala-143,	Asn-220 to Val-226.	Lys-49 to Trp-55,	Tyr-66 to Val-79,	Arg-89 to Asp-106,
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GIn-13/ to Asn-142.	Pro-1 to Arg-15,	Lys-49 to Trp-55,	Tyr-66 to Val-79,	Arg-89 to Asp-106,	Gln-137 to Asn-142,	Ala-171 to Tyr-178,	Glu-224 to Ser-231.	Met-17 to Met-24,	Ser-31 to Asp-37,	Leu-70 to Asp-97.														•	
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								X-					Met-14 to Met-21,	Ser-28 to Asp-34,	Leu-67 to Asp-94,	Ala-109 to Ile-123.	Val-9 to Arg-14,	Glu-22 to Phe-30,	Met-48 to Ser-59,	Thr-76 to Lys-81,	Ala-99 to Asp-104,	Lys-122 to Val-144,	Pro-159 to Glu-164,	Gly-169 to His-183,	Thr-188 to Asp-194,
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Lys-211 to Phe-218,	Ser-230 to Pro-236, S	Ala-276 to Glu-281,	Arg-297 to His-316, S	Ser-330 to Ser-335, I	Ser-367 to Thr-376, S	Pro-383 to Cys-394.				. .				<u> </u>	1	Val-9 to Arg-14,	Glu-22 to Phe-30.	Asn-38 to Tyr-46,	Pro-56 to Asp-71,	Asn-84 to Cys-96,	Ser-110 to Val-142,	Arg-181 to Leu-187,	His-193 to Gly-198,	Thr-201 to Arg-210,	Asn-224 to Leu-230,
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H0648: 3, L0747: 3,	L0749: 3, H0341: 2,	S0420: 2, S0356: 2,	S0354: 2, S0222: 2,	H0013: 2, H0575: 2,	L0738: 2, H0046: 2,	S0051: 2, S0003: 2,	H0551: 2, H0413: 2,	H0056: 2, H0529: 2,	L0768: 2, L0794: 2,	L0666: 2, H0547: 2,	L0750: 2, L0779: 2,	L0758: 2, L0686: 2,	L0593: 2, S0412: 2,	H0170: 1, L0441: 1,	H0685: 1, H0381: 1,	H0305: 1, S0007: 1,	H0619: 1, S6026: 1,	H0549: 1, H0550: 1,	S6014: 1, H0586: 1,	H0333: 1, H0559: 1,	T0039: 1, H0156: 1,	H0098: 1, H0036: 1,	H0505: 1, H0327: 1,	S0050: 1, H0051: 1,	S0388: 1, T0010: 1,
Thr-246 to Gly-251,	Ser-267 to Ser-272,	Ser-284 to Gln-290,	Asp-294 to Asn-301,	Asp-318 to Asn-324,	Asn-338 to Glu-343,	Gln-353 to Glu-362,	Lys-374 to Lys-381,	Asn-397 to Ala-409,	Pro-426 to Tyr-436,	Thr-469 to Pro-474,	Ile-486 to Asn-492,	Ile-499 to Ile-505,	Lys-531 to Gln-539,	Lys-585 to His-592,	Lys-627 to Gly-635.							-			
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																				Asn-38 to Tyr-46,	Pro-56 to Asp-71,	Asn-84 to Cys-96,	Ser-110 to Val-142,	Arg-181 to Leu-187,	His-193 to Gly-198,
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Thr-201 to Arg-210,	Asn-224 to Leu-230,	Thr-246 to Gly-251,	Ser-267 to Ser-272,	Ser-284 to Gln-290,	Asp-294 to Asn-301,	Asp-318 to Asn-324,	Asn-338 to Thr-347.	Asn-1 to Ser-7,	Leu-9 to Asn-16,	Ser-48 to Gln-55,	Arg-136 to Pro-141,	Ala-144 to Lys-151.	Asp-1 to Ser-7,	Pro-10 to Cys-18,	Glu-36 to Ala-54,	Tyr-83 to Pro-91,	Pro-108 to Gly-115.	Asn-1 to Ser-7,	Leu-9 to Asn-16,	Ser-48 to Gln-55,	Arg-136 to Pro-141,	Ala-144 to Lys-151.		Pro-19 to Cys-27,	Glu-45 to Ala-63,
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	Asp-96 to Pro-102,	Pro-117 to Gly-124,	Pro-132 to Ser-143.	Arg-23 to Thr-29,	Gly-45 to Arg-51,	Pro-56 to Glu-66.		Arg-8 to Pro-15,	Gly-37 to Arg-46,	Lys-59 to Leu-67,	Ala-108 to Asp-113.	Arg-10 to His-17,	Gln-24 to Asn-29,	Glu-42 to His-51,	Glu-63 to Asp-70,	His-78 to Arg-84,	Lys-101 to Phe-106,	Phe-171 to Ser-180,	Lys-182 to Gln-189,	Pro-191 to Thr-197,	Glu-236 to Ala-241,	Gly-250 to Asn-256,	Ser-293 to Ser-301,	Lys-320 to Leu-325,	Glu-334 to Val-340,	Asp-453 to Gly-466,
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Pro-473 to Asp-478,	Leu-576 to Lys-585.	Tyr-114 to Trp-119,	Gln-124 to Ile-129.	Asp-1 to Arg-7,	Glu-19 to Leu-32,	Leu-36 to Ser-49,	Ser-74 to Pro-100,	Ser-113 to Val-130,	Thr-143 to His-154,	Gln-161 to Arg-167,	Val-194 to Phe-200.	Asp-1 to Arg-7,	Glu-19 to Leu-32,	Leu-36 to Ser-49,	Ser-74 to Pro-100,	Ser-113 to Val-130,	Thr-143 to His-154,	Gln-161 to Arg-167,	Val-194 to Phe-200.	Cys-52 to Trp-57,	Pro-69 to Asp-74,	Glu-95 to Ser-115,	Pro-136 to Gly-143.		
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L0809: 1, H0648: 1 and	L0748: 1.		AR089: 6, AR061: 4	H0561: 2, S0002: 2,	H0521: 2, H0522: 2,	H0656: 1, H0341: 1,	H0550: 1, T0040: 1,	H0036: 1, H0031: 1,	H0560: 1, S0152: 1 and	H0134: 1.				,						. `	•				
		Glu-48 to Leu-53.	Ser-3 to Trp-9,	Arg-12 to Ser-18,	Asp-42 to Gln-53,	Arg-79 to Gly-90,	Val-103 to Asp-108,	Gly-175 to Asn-193,	Ser-210 to Thr-217,	Lys-242 to Glu-251,	Glu-267 to Lys-273,	Leu-287 to Lys-293,	Ser-311 to Glu-318,	Pro-335 to Lys-364,	Asn-370 to Glu-376,	Ala-392 to Thr-401.	Ser-3 to Trp-9,	Arg-12 to Ser-18,	Asp-42 to Gln-53,	Arg-79 to Gly-90,	Val-103 to Asp-108,	Gly-175 to Asn-193,	Ser-210 to Thr-217,	Lys-242 to Glu-251,	Glu-267 to Lys-273,
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Leu-287 to Lvs-293.	Ser-311 to Glu-318,	Pro-335 to Lys-364,	Asn-370 to Glu-376,	Ala-392 to Thr-401.	Glu-6 to Asp-20,	Thr-25 to Lys-31,	Lys-73 to Ala-95,	Glu-102 to Phe-109,	Pro-112 to Pro-118,	Asp-136 to Leu-152,	Val-246 to Thr-253,	Thr-298 to Glu-303,	Val-312 to Arg-322,	Pro-341 to Arg-349,	Lys-378 to Phe-388,	Val-392 to Ala-397.	-						·		
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H0591: 1, H0646: 1, S0002: 1, L0772: 1, L0645: 1, L0773: 1, L0662: 1, L0794: 1, L0776: 1, L0776: 1, L0659: 1, L0659: 1, L0666: 1, L0790: 1, L0666: 1, H0547: 1, H0648: 1, H0539: 1, S0152: 1, H0696: 1, S0011: 1, S0028: 1, L0758: 1, L0366: 1, S0011: 1, S0276: 1, H0422: 1 and S0424: 1.		AR089: 4, AR061: 2 S0212: I and H0555: 1.	AR089: 4, AR061: 1
	Pro-25 to Arg-32, Met-56 to Ser-75, Asn-90 to Trp-95, Lys-111 to Arg-121, His-134 to Arg-140, Arg-153 to Gln-162, Gln-169 to Gly-186.	Phe-16 to Asp-22, Val-93 to Gly-98. Pro-6 to Arg-12.	Leu-9 to Gln-17,
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Leu-27 to Arg-42,	Leu-51 to Ser-58,	Ser-66 to Ser-74,	Asn-79 to Ala-85,	Ser-90 to Phe-102,	His-128 to Gly-143,	Pro-158 to Lys-167.				,														Leu-6 to Gln-14,	Leu-24 to Arg-39,
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Leu-48 to Ser-55, Ser-63 to Ser-71	Asn-76 to Ala-82,	Ser-87 to Phe-99,	His-125 to Gly-140,	Pro-160 to Asp-165.	Gln-1 to Pro-29.															-				
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		Asn-11 to Pro-18, Tyr-31 to Asp-36, Asp-98 to Ser-119, Asp-142 to Glu-155, Gly-215 to Ile-226, Ser-237 to Ser-251, Leu-255 to Arg-260, His-263 to Asn-270,
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H0662: 1, S0354: 1,	H0549: 1, S0665: 1,	T0048: 1, L0157: 1,	H0031: 1, H0038: 1,	S0002: 1, L0761: 1,	L0800: 1, L0806: 1,	L0787: 1, H0660: 1,	S0330: 1, L0602: 1,	S0206: 1, L0745: 1,	L0756: 1, L0752: 1,	L0759: 1, L0591: 1 and	H0543: 1.										AR089: 11, AR061: 7	H0253: 2, L0439: 1	and L0599: 1.		
Lys-287 to Thr-295.												Asn-11 to Pro-18,	Tyr-31 to Asp-36,	Asp-98 to Ser-119,	Asp-142 to Glu-155,	Gly-215 to Ile-226,	Ser-237 to Ser-251,	Leu-255 to Arg-260,	His-263 to Asn-270,	Lys-287 to Thr-295.	Trp-3 to Thr-14,	Ala-21 to Arg-30,	Glu-66 to Pro-74,	Pro-103 to Gly-108,	He-135 to He-142,
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	Thr-185 to Asp-210,	Leu-283 to Leu-297,	Trp-328 to Leu-334.	Gly-3 to Ser-8.	Asn-20 to Tyr-32,	Gly-41 to Arg-54.					,															
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	-	•		Gly-9 to Thr-14,	Lys-37 to Arg-42,	Asp-47 to Ser-54,	Asp-58 to Lys-63,	Lys-82 to Asn-89.	Tyr-17 to Val-23,	Ala-54 to Leu-65,	Arg-115 to Asn-120,	Ser-150 to Ser-158,	Glu-234 to Ile-251,	His-272 to Asn-277,	Gly-284 to Gln-303,	Glu-327 to Lys-332,	Thr-362 to Leu-368,	Leu-390 to Asn-399,	Ser-432 to Tyr-444,	Asn-456 to Thr-467,	Ser-474 to Thr-484,	Asn-505 to Leu-510,	Gln-563 to Ser-568,	Ala-575 to Cys-582.	Tyr-14 to Phe-24.
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4.	Pro-1 to Gln-11,	Leu-36 to Gln-42,	Glu-81 to Trp-86,	Arg-108 to Lys-113,	Arg-143 to Asn-149,	Glu-154 to Asp-160,	Glu-169 to His-174,	Trp-184 to Ser-189,	Lys-210 to Trp-217,	Lys-233 to Tyr-239,	Asp-308 to Gly-315.		,		Gly-8 to Gly-15,	Ser-25 to Ser-30,	Glu-65 to Ala-71.								
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	Arg-15 to Leu-23, Glu-70 to Lys-76, Lys-96 to Gln-102,	Leu-119 to Arg-124, Ala-141 to Glu-146,	Leu-159 to Glu-169, Thr-195 to Lys-202	Gln-239 to Gly-251.			Gly-1 to Lys-8,	Arg-52 to Gly-57,	Asp-69 to Ser-74,	Asp-126 to Thr-132,	Cys-155 to Thr-171,	Lys-189 to Ala-198,	Lys-239 to Ser-245,	Gln-260 to Ser-276,
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Ser-295 to Glu-302,	Asp-307 to Leu-319,	Ser-332 to Leu-347,	Ser-363 to Ala-371,	Ser-429 to Asp-436,	Ala-458 to Asn-463,	Pro-477 to Asn-483,	He-587 to Tyr-594,	Lys-603 to His-611,	Pro-620 to Ser-625,	Lys-661 to Trp-677,	Glu-700 to Glu-714.											-			
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											,		Arg-44 to Gly-49,	Asp-61 to Ser-66,	Asp-73 to His-78.	Leu-39 to Tyr-45,	Ser-57 to Ser-63,	Thr-74 to Leu-82,	Pro-91 to Asp-98.	Asp-40 to Leu-46,	Phe-50 to Arg-61,	Pro-76 to Asp-83.				
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				:		-	Lys-1 to Thr-7,	Arg-34 to Pro-41.	Gly-2 to Asp-11,	Ser-71 to Gln-78,	Ser-110 to Asn-117,	Ser-155 to Ser-162,	Thr-171 to Asp-181,	Arg-193 to Leu-203,	Arg-207 to Thr-215,	Ala-225 to Lys-246,	Lys-248 to Leu-255.	Ser-12 to Gln-19,	Ser-51 to Asn-58,	Ser-96 to Ser-103,	Thr-112 to Asp-122,	Arg-134 to Leu-144,	Arg-148 to Thr-156,	Ala-166 to Lys-187,	Lys-189 to Gly-200.
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0.	Asp-2 to Asn-11.	Ala-5 to Gly-18.				Pro-1 to Tyr-7,	Glu-14 to Ser-21,	Pro-23 to His-31,	Pro-33 to Gly-38,	Thr-82 to Arg-87,	Val-91 to Gly-96.		-			-									
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H0633: 1, S0144: 1,	S0426: 1, L0639: 1,	L0637: 1, L0761: 1,	L0646: 1, L0644: 1,	L0764: 1, L0766: 1,	L0803: 1, L0775: 1,	L0375. 1, L0652: 1,	L0655: 1, L0384: 1,	L0382: 1, L0663: 1,	L0664: 1, L'0665: 1,	S0052: 1, H0144: 1,	H0547: 1, L0741: 1,	L0743: 1, L0740: 1,	L0750: 1, H0595: 1,	L0588: 1, L0601: 1,	S0276: 1, H0423: 1,	H0422: 1 and H0352: 1.		AR089: 43, AR061: 8	H0592: 2, H0009: 1,	H0030: 1, L0143: 1,	H0264: 1, H0646: 1,	L0653: 1, L0665: 1,	S0052: 1 and H0658: 1.	-	
		*							٠	-							Pro-107 to Arg-120.	Arg-11 to Pro-17,	Glu-43 to Gln-50,	Gln-74 to Gln-85,	Leu-127 to Asn-132,	Arg-141 to Lys-146.		Arg-11 to Pro-17,	Glu-43 to Gln-50,
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	AR089: 4, AR061: 1	L0794: 3, L0803: 3,	L0809: 3, S0222: 2,	L0747: 2, L0756: 2,	L0752: 2, L0758: 2,	H0171: 1, L0002: 1,	S0420: 1, S6026: 1,	H0427: 1, L0021: 1,	H0051: 1, T0010: 1,	H0032: 1, S0422: 1,	L0775: 1, L0659: 1,	L0367: 1, L0790: 1,	L0666: 1, L0744: 1,	L0754: 1, L0779: 1,	L0777: 1 and L0757: 1.		AR089: 1	S0002: 2 and H0522: 1.			*			AR089: 8, AR061: 2	L0759: 15, L0766: 9,
Gln-74 to Gln-85.	Glu-1 to Gly-6,	Glu-50 to Val-55,	Tyr-62 to Leu-67,	Glu-105 to Lys-113,	Ser-127 to Val-132,	Ala-141 to Val-146,	Thr-154 to Leu-159,	Leu-170 to Ser-177,	Pro-182 to Asn-194.								Gly-38 to Pro-48,	Pro-105 to Ser-116,	Arg-120 to Ser-127,	Ser-142 to Ser-149.	Ala-14 to Gly-20,	Gly-34 to Pro-44,	His-128 to Ser-134.	Glu-58 to Ala-72,	Thr-91 to Gln-98,
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L0754: 8, L0769: 6,	S0126: 6, L0439: 6,	S0360: 5, L0776: 5,	S0027: 5, L0731: 5,	H0556: 4, H0341: 4,	H0641: 4, L0747: 4,	L0750: 4, L0596: 4,	L0588: 4, H0650: 3,	Н0637: 3, Н0013: 3,	H0644: 3, H0412: 3,	H0560: 3, L0809: 3,	S0330: 3, H0521: 3,	L0742: 3, H0543: 3,	H0624: 2, H0171: 2,	S0134: 2, H0656: 2,	S0354: 2, S0007: 2,	H0351: 2, H0333: 2,	H0492: 2, H0599: 2,	H0618: 2, H0581: 2,	H0620: 2, S0051: 2,	T0010: 2, H0594: 2,	H0628: 2, H0090: 2,	H0591: 2, H0264: 2,	T0042: 2, L0641: 2,	L0794: 2, L0774: 2,	L0527: 2, L0659: 2,
Glu-106 to Glu-115,	Gln-128 to Asp-134,	Lys-143 to Lys-148,	Lys-170 to Ser-178,	Ser-183 to Gly-190.						,								,							
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L0564: 1, H0022:	S0150: 1, H0633:	S0144: 1, L0770:	L0637: 1, L0761:	L0646: 1, L0764:	L0773: 1, L0662:	L0768: 1, L0381:	L0803: 1, L0775.	L0651: 1, L0653:	L0783: 1,	L0791: 1, L0792: 1	L0663: 1, S0428:	L0438: 1, H0547:	H0659: 1, H0658:	H0670: 1, H0672:	H0539: 1, H0518:	H0436: 1, S3014:	L0740: 1, L0751:	L0777: 1, L0780:	L0752: 1, L0755:	H0444: 1	H0343: 1, L0592:	H0667: 1	S0192: 1, S0194: 1	H0542: 1	
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Tyr-63 to Ala-72,	Thr-91 to Gln-98,	Glu-106 to Glu-115,	Gln-128 to Asp-134,	Lys-143 to Lys-148,	Lys-170 to Ser-178,	Ser-183 to Gly-190.	Arg-1 to Pro-12,	Pro-18 to Lys-25,	Arg-28 to Cys-38,	Val-61 to Leu-67,	Pro-84 to Ser-95.														
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H0375: 1, H0594:	H0687: 1, H0553:	H0644: 1, L0055:	H0383: 1, H0169: 1	H0064: 1, H0708: 1,	H0068: 1, H0598:	H0135: 1, H0038:	H0616: 1, H0413: 1	H0056: 1, S0112: 1,	L0564: 1, H0280: 1	H0494: 1, H0625:	H0561: 1, S0344: 1	H0538: 1, L0763:	L0761: 1, L0772:	L0646: 1, L0800:	L0773: 1, L0662:	L0794: 1, L0650:	L0651: 1, L0806:	L0654: 1, L0528:	L0663: 1, H0144:	S0374: 1, H0520:	H0682: 1, H0659: 1	H0660: 1, H0648:	S0328: 1, S0330:	H0539: 1, S0380: 1	H0518: 1, S0146: 1,
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S0432: 1, S0390: 1, S0027: 1, L0750: 1, L0752: 1, L0757: 1, S0031: 1, H0445: 1, L0684: 1, L0592: 1, L0485: 1, L0608: 1, L0594: 1, S0026: 1, H0423: 1, H0422: 1, S0042: 1 and L0698: 1.		AR089: 22, AR061: 3 H0486: 2, H0635: 1, H0052: 1, H0634: 1, L0748: 1 and H0444: 1.
	Pro-1 to Pro-7, Pro-13 to Lys-20, Arg-23 to Cys-33, Val-56 to Leu-62, Pro-79 to Ser-90, Thr-169 to Gly-175, Thr-186 to Asn-192, Asp-200 to Pro-207, Lys-248 to Val-253, Lys-248 to Cys-305. Leu-294 to Cys-305.	Leu-4 to Thr-25, Thr-52 to Gln-57, Gly-111 to Ser-118, Pro-149 to Lys-158. Leu-4 to Thr-25, Thr-52 to Gln-57,
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Ser-95 to Gly-103,	Thr-114 to Asn-120.	Gln-6 to Asp-13,	Thr-68 to Leu-80,	Arg-130 to Thr-135,	Pro-189 to Ser-201.								·					,							
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Cys-14 to Lys-31,	Thr-87 to Leu-99,	Arg-149 to Thr-154, Pro-208 to Ser-220.	Glu-37 to Thr-42,	Leu-127 to Glu-132,	Ser-175 to Cys-183.												,				,			
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							Glu-37 to Thr-42.	Lys-35 to Val-45,	Ser-133 to Ala-138,	Asp-162 to Asp-174,	Gln-179 to Cys-186,	Arg-214 to Pro-223.		٠	•											
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Thr-158 to Gly-163, Gly-195 to Tyr-201.	Tyr-1 to Asp-11, Asp-64 to His-73,	Ala-90 to Gly-100, Ile-133 to Asn-138,	Val-195 to His-213.														Tyr-1 to Asp-11,	Asp-64 to His-73,	Ala-90 to Ile-96.	Ile-3 to Thr-11,	Asn-31 to Lys-40,
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Asn-44 to Val-53.			,																						
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	Ala-19 to Phe-24,	Thr-45 to Val-53,	Ile-77 to Arg-83,	Ser-105 to Gly-111,	Gln-128 to Ala-144,	Asp-153 to Gly-161.				Thr-3 to Arg-10,	Lys-71 to Lys-80,	Glu-107 to Arg-120,	Lys-128 to Gly-133.												
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	Gln-21 to Ala-28,	Tyr-55 to Phe-60,	Tyr-78 to Ile-84.		Gln-21 to Ala-28,	Tyr-55 to Phe-60,	Tyr-78 to Ile-84.	Pro-7 to Ile-20,	Arg-26 to Trp-36,	Trp-68 to Thr-88,	Pro-96 to Gly-101,	Ser-109 to Arg-117,	Pro-163 to Ala-169,	Asp-260 to Asp-266.				-							
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														Asn-40 to Asn-47,	Ala-74 to Gly-89,	Thr-100 to Asn-106,	Gly-129 to Glu-139,	Ile-182 to Gly-193,	Arg-204 to Ser-211.	Phe-49 to Lys-55.				
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		Asp-14 to Ile-20.	Pro-10 to Gly-15,	Lys-80 to Ile-88,	Gly-161 to Tyr-169,	Arg-175 to Arg-183.		,				Gln-1 to Gly-13,	Thr-57 to Phe-63,	Gln-84 to Tyr-89,	Glu-98 to Pro-104,	Tyr-161 to Phe-168,	Leu-181 to Glu-202.	Tyr-1 to Asp-11,	Asp-64 to His-73,	Ala-90 to Gly-100,	Ile-133 to Asn-138,	Val-195 to His-213.	
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	lle-12 to Asn-17, Val-74 to His-92.	Asp-47 to Ser-53, Ala-82 to Arg-88. Asp-47 to Ser-53, Ala-82 to Thr-89.	Pro-17 to His-22. Gln-60 to Ala-68, Trp-132 to Ser-138, Lys-156 to Val-163.
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	AR089: 9, AR061:	S0358: 10, L0747: 7,	L0750: 7, L0731: 7,	H0620: 5, L0659: 5,	S0360: 4, S0022: 4,	L0666: 4, L0665: 4,	L0748: 4, L0740: 4,	L0777: 4, L0757: 4,	L0588: 4, H0265: 3,	S0420: 3, H0046: 3	H0135: 3, H0100: 3,	L0650: 3, L0375: 3	L0382: 3, H0651: 3,	S0028: 3, L0755: 3,	H0352: 3, S0278: 2,	H0592: 2, H0333: 2,	H0253: 2, H0544: 2,	H0123: 2, H0081: 2,	H0012: 2, H0252: 2,	H0428: 2, L0763: 2,	L0770: 2, L0774: 2,	L0518: 2, L0809: 2,	H0682: 2, S0037: 2,	S0027: 2, L0751: 2,	L0758: 2, H0170: 1,
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	Arg-12 to Leu-19,	Gly-56 to Pro-62,	Cys-68 to Gly-74,	Phe-100 to Lys-110,	Ala-137 to Phe-142,	Leu-179 to Ser-185,	Ala-278 to Cys-285.					-					•								-
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						.·		-		Arg-12 to Leu-19,	Gly-56 to Pro-62,	Cys-68 to Gly-74,	Phe-100 to Lys-110,	Ala-137 to Phe-142,	Leu-179 to Phe-185.	Thr-1 to Gln-18,	Thr-55 to His-60,	Ala-91 to Gln-102,	Ser-117 to His-124,	Val-132 to Gly-139,	Lys-148 to Gly-158,	Glu-220 to Lys-234,	Gln-253 to Gly-260,	Asp-274 to Pro-281,	Gln-318 to Val-326,
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Pro-334 to Glu-344, Gln-382 to Pro-389.	Arg-1 to Gln-15, Thr-52 to His-57, Ala-88 to Gln-99,	Ser-114 to His-121, Val-129 to Gly-136.	Val-49 to Gln-56,	Ala-85 to Leu-93,	Pro-96 to Ala-101,	Val-110 to Asn-118,	Asp-131 to Glu-136,	Lys-146 to Ala-159,	Met-164 to Tyr-169,	Thr-174 to Thr-180.	Val-49 to Gln-56,	Ala-85 to Leu-93,	Pro-96 to Ala-101,	Val-110 to Asn-118,	Asp-131 to Glu-136,	Lys-146 to Ala-159,
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Met-164 to Tyr-169,	Thr-174 to Thr-180,	Ser-213 to Gly-218.	Ala-1 to Met-18,	Leu-20 to Asn-26,	Val-38 to Leu-46,	Pro-48 to Gly-53,	Leu-81 to Gly-86,	Gln-94 to Tyr-99,	Glu-101 to Gly-109.	,				Pro-9 to Gln-16,	Phe-31 to Tyr-40,	Gln-61 to Trp-66,	Arg-71 to Gln-78,	Gly-86 to Arg-92.	Gln-1 to Ala-7,	Thr-36 to Trp-42,	Gly-45 to Gly-52,	Glu-77 to Pro-89,	Gly-105 to Gly-132,	Ser-135 to Glu-162.	
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H0545: 4, H0024: 4	S0354: 3, H0250: 3,	H0123: 3, H0031: 3,	L0659: 3, S0328: 3,	L0731: 3, H0583: 2,	L0808: 2, L0785: 2,	H0662: 2, H0586: 2,	H0618: 2, H0253: 2,	H0424: 2, H0264: 2,	H0488: 2, Ĥ0100: 2,	L0771: 2, L0806: 2,	L0809: 2, H0144: 2,	H0689: 2, L0749: 2,	L0750: 2, L0779: 2,	L0777: 2, H0707: 2,	L0595: 2, H0624: 1,	H0341: 1, S0356: 1,	S0360: 1, H0619:	H0411: 1, H0370: 1	H0485: 1, H0635:	H0025: 1, H0108:	H0318: 1, H0581:	T0110: 1, H0231:	L0738: 1, H0086:	H0271: 1, T0006: 1,	H0644: 1, H0181:
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								Gly-12 to Gly-31,	Asn-38 to Gly-62,	Asp-70 to Phe-84,	Val-94 to Ser-101,	Ala-112 to Ser-125,	Lys-140 to Asn-145,	Asn-175 to Tyr-180,	Arg-187 to Thr-192.					Val-1 to Lys-8,	Pro-36 to Lys-41,	Gln-49 to Lys-57,	Ser-63 to Ser-70,	Asp-79 to Gln-92,	Asn-103 to Thr-122.
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Arg-4 to Val-12,	Glu-19 to Arg-29,	Glu-34 to Arg-76.		-					3-		Glu-5 to Arg-15,	Glu-20 to Arg-62.	Gln-22 to Asp-41,	Pro-49 to Thr-58,	Leu-99 to Gly-107,	Ala-117 to Ala-122,	Gln-128 to Trp-134,	Pro-136 to Pro-144,	Phe-147 to Glu-153,	Glu-183 to Val-188,	Glu-195 to Glu-200,	Glu-257 to Leu-265,	Met-275 to Ser-283.	Gln-19 to Asp-38,	Pro-46 to Thr-55,
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Leu-96 to Gly-104, Ala-114 to Ala-119, Gln-125 to Trp-131, Pro-133 to Pro-141,	Phe-144 to Glu-150, Glu-180 to Val-185,	Glu-192 to Glu-197,	Glu-254 to Leu-262, Met-272 to Ser-280.	Asp-43 to Glu-48.	,	*			is .					Pro-1 to Gly-6,	Ala-41 to Leu-47.	Pro-1 to Glu-15,	Ala-26 to Lys-32,	Glu-46 to Leu-65,	Arg-82 to Cys-94,	Leu-101 to Glu-107,
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	Asp-1 to Glu-11,	Ala-22 to Lys-28,	Glu-42 to Leu-61,	Arg-78 to Cys-90,	Leu-97 to Glu-103.	Arg-17 to Leu-34,	Asp-44 to Ser-51,	Asp-63 to Gly-72,	Pro-74 to Gly-83,	Thr-97 to Met-102.					,		-							
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		Lys-7 to Gly-69,	Lys-82 to Lys-88,	Ser-94 to Asp-112,	Ala-126 to Asp-131,		Ser-147 to Phe-156,		Thr-176 to Asp-186,	Glu-230 to Leu-250,	Glu-291 to Arg-298,	Gln-313 to Glu-320,	Asn-331 to Gly-343,	Ser-348 to Leu-363.				-		-					·
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L0779: 1, H0445: 1 and	S0424: 1.	AR050: 48, AR054:	42, AR051: 35, AR089:	3, AR061: 1	H0575: 2, H0580: 1,	S0002: 1, S0426: 1,	H0521: 1, H0436: 1 and	L0748: 1.	AR054: 60, AR051:	40, AR050: 36, AR089:	5, AR061: 2	H0521: 4, H0486: 2,	S0002: 2, L0770: 2,	L0769: 2, L0766: 2,	L0518: 2, L0783: 2,	L0777: 2, L0731: 2,	H0422: 2, H0556: 1,	H0583: 1, H0650: 1,	H0657: 1, H0179: 1,	L0055: 1, H0488: 1,	S0426. 1, L0662: 1,	L0775: 1, L0655: 1,	L0665: 1, S0053: 1,	H0659: 1, L0754: 1,	L0779: 1, L0759: 1 and
		Leu-31 to Ser-39,	Val-57 to Trp-63,	Pro-103 to Gln-111,	Leu-118 to Leu-124.				Ser-60 to Thr-71,	Thr-82 to Leu-94,	Gln-113 to Asp-123,	Val-125 to Tyr-133,	Leu-144 to Gly-149.												
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H0543: 1.	AR061: 7, AR089: 4	H0100: 1 and H0521:											AR089: 6, AR061: 4	L0754: 6, L0777: 6,	L0740: 5, L0731: 4,	L0758: 4, L0759: 4,	S0001: 3, S0280: 3,	L0770: 3, L0764: 3,	L0747: 3, L0749: 3,	L0366: 3, S0412: 3,	S0007: 2, H0411: 2,	H0013: 2, L0471: 2,	T0004: 2, L0598: 2,	L0638: 2, L0662: 2,	L0783: 2, L0438: 2,
	Gln-13 to Ser-18,	Glu-32 to Gly-37,	Ala-44 to Trp-49,	Glu-56 to Val-61,	Gln-68 to Lys-74,	Ala-83 to Glu-88,	Arg-111 to Gly-117,	Tyr-123 to His-143,	Ser-167 to Thr-202.	Gln-13 to Ser-18,	Glu-32 to Gly-37,	Ala-44 to Trp-49.	Val-30 to Ser-37,	Gln-43 to Asp-62,	Pro-74 to Glu-79,	Thr-102 to Phe-109.									
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H0696: 2, L0744: 2,	L0748: 2, L0751: 2,	L0745: 2, L0779: 2,	L0752: 2, H0170: 1,	S0282: 1, H0662: 1,	H0574: 1, T0060: 1,	H0427: 1, H0590: 1,	S0010: 1, L0105: 1,	S0049: 1, H0194: 1,	H0373: 1, L0163: 1,	H0201: 1, H0031: 1,	H0553: 1, S0306: 1,	L0776: 1, L0659: 1,	L0526: 1, L0809: 1,	L0663: 1, H0144: 1,	H0547: 1, H0648: 1,	H0672: 1, L0743: 1,	L0780: 1, S0031: 1,	H0343: 1, L0604: 1 and	H0653: 1.	AR061: 16, AR089: 6	L0804: 1, S0052: 1,	H0144: 1 and H0659: 1.	AR089: 18, AR061: 5	L0740: 11, L0439: 9,	L0748: 8, H0616: 5,
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L0666: 5, L0601: 5,	S0444: 4, L0776: 4,	L0659: 4, L0744: 4,	L0747: 4, L0749: 4,	L0755: 4, H0457: 3,	L0774: 3, L0750: 3,	H0624: 2, T0002: 2,	S0116: 2, S0358: 2,	H0550: 2, T0040: 2,	H0013: 2, H0599: 2,	H0050: 2, H0673: 2,	H0038: 2, H0040: 2,	H0494: 2, L0770: 2,	L0662: 2, L0364: 2,	L0375: 2, L0809: 2,	L0438: 2, H0547: 2,	L0754: 2, L0756: 2,	L0752: 2, L0731: 2,	L0758: 2, L0485: 2,	S0040: 1, H0583: 1,	H0650: 1, H0657: 1,	H0341: 1, H0663: 1,	H0580: 1, H0619: 1,	L0717: 1, H0574: 1,	H0052: 1, H0263: 1,	H0009: 1, H0172: 1,
Tyr-85 to Asp-91,	Glu-100 to Glu-109.		,			·					.*							,				-			
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H0024: 1, T0010: 1,	H0510: 1, H0644: 1,	S0036: 1, H0551: 1,	H0264: 1, H0488: 1,	H0056: 1, H0100: 1,	L0564: 1, T0041: 1,	H0652: 1, S0344: 1,	S0002: 1, L0763: 1,	L0638: 1, L0761: 1,	L0372: 1, L0643: 1,	L0764: 1, L0768: 1,	L0381: 1, L0775: 1,	L0526: 1, L0782: 1,	L0663: 1, L0665: 1,	H0703: 1, H0520: 1,	H0435: 1, H0521: 1,	S0044: 1, L0751: 1,	L0757: 1, L0759: 1,	H0445: 1, L0584: 1,	L0608: 1 and H0506: 1.						S0007: 2, L0794: 2,
										,	- X									Gly-11 to Thr-16,	Ser-35 to Ser-56,	Thr-58 to Ser-73,	Tyr-85 to Asp-91,	Glu-100 to Glu-109.	Ser-6 to Trp-24.
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S0434: 2, S0354: 1,	N0006: 1, H0622: 1 and	H0478: 1.	AR089: 3, AR061: 2	H0563: 1 and H0123:	 AR089: 3, AR061: 1	T0042: 1, H0543: 1	and H0422: 1.	AR089: 3, AR061: 2	L0666: 8, L0439: 6,	H0253: 5, H0046: 4,	L0769: 4, H0295: 3,	H0255: 3, L0747: 3,	L0756: 3, L0779: 3,	H0657: 2, H0618: 2,	H0318: 2, H0622: 2,	H0068: 2, L0667: 2,	L0772: 2, L0776: 2,	L0663: 2, H0520: 2,	H0593: 2, H0670: 2,	H0521: 2, L0750: 2,	L0759: 2, L0593: 2,	L0601: 2, S0116: 1,	H0341: 1, S0212: 1,	H0306: 1, H0402: 1,
					Leu-7 to Phe-27,	Gln-50 to Gln-57.		Tyr-47 to Glu-58,	Lys-70 to Gly-77,	Pro-121 to Leu-126,	Leu-150 to Leu-158,	Asn-166 to Glu-171,	Arg-417 to Ser-425,	Phe-465 to Cys-473,	Ser-485 to Asn-492,	Ser-497 to Ala-504,	Gln-531 to Trp-537,	Asp-557 to Glu-562.						-
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L0617: 1, S0358:	H0609: 1, H0592: 1	H0333: 1, T0040: 1	H0013: 1, H0635: 1	H0575: 1, H0036: 1	I: 1, H(): 1, H(H0071: 1, T0010: 1	H0687: 1, H0290: 1	Н0617: 1, Й0606: 1	H0038: 1, H0487:	H0494: 1, H0334: 1	S0150: 1, H0647: 1	S0142: 1, L0640:	L0639: 1, L0637:	L0641: 1, L0768:		L0659: 1, L0783:	L0788: 1, L0664:	L0665: 1, L0438:	': 1, H0	: 1, HO	S0404: 1, H0478:	L0742: 1, L0740:	L0749: 1, L0758: 1	S0434: 1, S0194:
L0617	H060	H033.	H001.	H057	H058	H005(H007	H0687	H0617	H0038	H049	S0150	S0142	T0639	L0641	L0649	F0659	L0788	T0665	H0547	H0522	S0404	L0742	L0749	S0434
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H0422: 1 and H0506: 1.	AR089: 2, AR061: 1	T0049: 1, S0278: 1,	H0031: 1 and H0539: 1.				AR089: 3, AR061: 3	S0358: 8, L0766: 7,	L0777: 7, L0731: 7,	L0659: 4, L0748: 4,	L0751: 4, L0783: 3,	L0663: 3, S0418: 2,	S0360: 2, H0486: 2,	S0010: 2, S0250: 2,	S0422: 2, L0763: 2,	L0803: 2, L0775: 2,	L0789: 2, H0520: 2,	L0756: 2, L0752: 2,	H0656: 1, S0376: 1,	H0208: 1, H0574: 1,	H0632: 1, S0414: 1,	H0581: 1, H0052: 1,	H0024: 1, H0014: 1,	H0355: 1, H0688: 1,	H0090: 1, H0623: 1,
	Ser-11 to Trp-16,	lle-20 to Trp-26,	Asn-37 to Ser-58,	Leu-67 to Gln-72,	Lys-101 to Asp-108,	Asp-135 to Tyr-140.	-																,		
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H0509: 1, H0529: 1,	L0520: 1, L0761: 1,	L0650: 1, L0809: 1,	L0666: 1, L0665: 1,	S0126: 1, H0684: 1,	H0648: 1, S0390: 1,	L0740: 1, L0745: 1,	L0749: 1, L0750: 1,	L0755: 1, L0591: 1,	L0362: 1 and S0242: 1.	AR051: 11, AR050: 9,	AR054: 5, AR089: 0,	AR061: 0	H0031: 5, S0222: 4,	S0028: 4, H0662: 3,	L0748: 3, S0260: 3,	S0276: 3, S0282: 2,	S0360: 2, S0046: 2,	H0575: 2, H0196: 2,	S0036: 2, H0268: 2,	L0662: 2, S0027: 2,	L0754: 2, L0747: 2,	L0749: 2, L0756: 2,	L0777: 2, L0604: 2,	L0595: 2, H0171: 1,	S0030: 1, S0029: 1,
										Thr-7 to Phe-29,	Thr-37 to Lys-52,	Glu-89 to Val-112.					-								
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S0358: 1, H0619: 1,	S0300: 1, L0717: 1,	H0550: 1, H0441: 1,	H0431: 1, H0392: 1,	T0060: 1, S0010: 1,	H0052: 1, H0309: 1,	\$6028: 1, \$0250: 1,	H0252: 1, H0553: 1,	S0364: 1, S0366: 1,	H0433: 1, H0269: 1,	H0412: 1, L0372: 1,	L0804: 1, L0789: 1,	L0666: 1, L0663: 1,	S0126: 1, S0044: 1,	H0345: 1, S0390: 1,	S0037: 1, S3014: 1,	L0743: 1, L0439: 1,	L0750: 1, L0779: 1,	L0599: 1, L0593: 1,	L0366: 1 and H0653: 1.	AR061: 1, AR089: 1	H0175: 1, H0266: 1,	H0292: 1, H0628: 1 and	L0779: 1.	AR089: 1, AR061: 1	S0002: 2 and L0766: 1.
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AR089: 2, AR061: 2	S0002: 2		AR089: 0, AR061: 0	H0583: 1, H0644: 1,	L0766: 1 and H0518: 1.	AR089: 4, AR061: 1	L0731: 7, L0517: 5,	S0212: 3, L0775: 3,	L0740: 3, H0266: 2,	L0809: 2, H0696: 2,	L0748: 2, S0132: 1,	H0574: 1, H0013: 1,	H0544: 1, H0023: 1,	H0071: 1, H0286: 1,	H0100: 1, H0494: 1,	S0370: 1, L0770: 1,	L0646: 1, L0764: 1,	L0771: 1, L0363: 1,	L0774: 1, L0659: 1,	L0789: 1, L0666: 1,	S0126: 1, H0522: 1,	L0754: 1, L0747: 1 and	L0755: 1.	AR050: 8, AR054: 6,	AR051: 3, AR089: 1,
Ser-11 to Ser-21,	Ser-84 to Ala-89,	Pro-98 to Arg-107.	He-26 to Trp-33,	Glu-52 to Leu-71.		-				,		0=0												Glu-9 to Ser-20,	Ile-23 to Gly-29,
734			735			736						•												737	
1 - 411			1 - 363			2 - 802			-				9											85 - 1557	
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AR061: 1	H0036: 2, L0766: 2,	H0686: 1, H0622: 1,	H0625: 1, L0791: 1,	L0779: 1 and S0434: 1.											,		AR089: 1, AR061: 0	H0457: 8, L0766: 7,	L0599: 6, H0677: 6,	L0438: 5, L0779: 5,	H0012: 3, L0809: 3,	H0656: 2, H0620: 2,	L0771: 2, H0435: 2,	H0436: 2, L0748: 2,	L0439: 2, L0751: 2,
Pro-50 to Cys-66,	Pro-74 to Glu-79,	Glu-93 to Trp-98,	Thr-121 to Ser-133,	Leu-180 to Lys-196,	Thr-213 to Glu-225,	Glu-234 to Glu-240,	Arg-263 to Glu-270,	Glu-283 to Ala-298,	Lys-318 to Ala-336,	Val-340 to Ala-351,	Val-361 to Pro-372,	Asn-445 to Pro-468,	Pro-475 to Lys-491.	Thr-1 to Ala-10,	Val-20 to Pro-31,	Asn-104 to Thr-124.	Lys-1 to Thr-34,	Phe-80 to Gly-85,	Tyr-91 to Ser-105,	Thr-122 to Ala-133,	Ser-151 to Ala-157,	Glu-208 to Trp-213,	His-219 to Trp-224,	Glu-237 to Glu-244,	Asn-251 to Ser-256,
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L0749: 2, S0134: 1,	H0645: 1, H0587: 1,	H0635: 1, H0581: 1,	H0546: 1, H0477: 1,	H0560: 1, H0641: 1,	S0422: 1, H0529: 1,	L0521: 1, L0662: 1,	L0794: 1, L0774: 1,	L0775: 1, L0606: 1,	L0659: 1, L0647: 1,	L0789: 1, L0791: 1,	L0792: 1, L0666: 1,	L0663: 1, L0665: 1,	H0702: 1, H0547: 1,	H0576: 1, S0028: 1,	L0756: 1, L0777: 1,	L0755: 1, L0758: 1,	H0543: 1 and H0506: 1.		AR089: 1, AR061: 0	S0040: 1, H0250: 1,	T0048: 1, L0761: 1,	L0764: 1, L0783: 1,	L0809: 1, L0789: 1 and	L0757: 1.	
Gln-291 to Trp-296,	Asn-311 to Phe-321,	Ser-327 to Glu-335,	Lys-364 to Trp-369,	Ala-376 to Gly-384,	Asn-437 to Trp-444,	Met-462 to Trp-472,	Gln-483 to Gly-491,	Thr-499 to Trp-504,	Arg-512 to Ala-517.	,								Glu-1 to Thr-13.	Pro-8 to Ser-13.						Thr-8 to Gln-19,
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-		AR089: 2, AR061: 1	L0794: 6, L0598: 2,	L0803: 2, L0748: 2,	S0040: 1, S0046: 1,	H0431: 1, H0318: 1,	L0766: 1, L0606: 1,	L0749: 1, L0758: 1 and	S0192: 1.	AR089: 1, AR061: 1	H0031: 2	AR089: 3, AR061: 2	H0394: 1 and L0589:		AR061: 6, AR089: 5	H0328: 4, H0031: 3,	L0519. 3, L0748: 2,	L0777: 2, L0731: 2,	S0260: 2, H0624: 1,	S6024: 1, H0650: 1,	S0116: 1, H0254: 1,	S0007: 1, H0393: 1,	H0441: 1, H0438: 1,	H0574: 1, H0156: 1,	H0599: 1, S0051: 1,
Lys-26 to Glu-33,	Lys-41 to Ile-50.	Lys-27 to Ile-43.					-			Met-43 to Trp-52.		Gln-36 to Ile-46,	Ser-55 to Phe-65,	Ser-67 to Lys-78.	His-13 to Gly-21,	Tyr-61 to Asp-66,	Ala-105 to Thr-110.								
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		160 - 846		,						191 - 346		190 - 456			202 - 540			of.							
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		HOUFT36	-							HPMFL08		HRSMD49			HSDII69										
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H0615: 1, H0039: 1,	L0564: 1, L0763: 1,	L0766: 1, L0774: 1,	L0776: 1, L0659: 1,	L0518: 1, L0792: 1,	L0666: 1, L0663: 1,	S0242: 1 and H0423: 1.	AR061: 4, AR089: 3	H0590: 7, L0754: 5,	H0156: 3, L0731: 3,	L0600: 3, S0360: 2,	H0339: 2, S0472: 2,	L0803: 2, L0751: 2,	L0779: 2, L0759: 2,	\$0031: 2, L0596: 2,	S0212: 1, H0411: 1,	S0222: 1, H0409: 1,	H0601: 1, H0333: 1,	H0632: 1, H0427: 1,	L0021: 1, H0037: 1,	H0596: 1, H0024: 1,	H0239: 1, S6028: 1,	H0266: 1, H0687: 1,	H0328: 1, H0644: 1,	H0674: 1, H0598: 1,	T0067: 1, H0509: 1,
						,	He-25 to Asn-36,	Glu-54 to Val-63,	Gly-81 to Glu-86,	Gly-108 to Thr-114,	Val-125 to Ser-131.														
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-	~									,					Leu-2 to Gly-8.		Arg-1 to Ser-8,	Lys-42 to Lys-48.			Pro-19 to Thr-24,	Thr-78 to Lys-89.	Glu-21 to Glu-27.		
															745		1132	-	746		747		1133	748	
									,		·				2 - 325		147 - 332		209 - 361	,	220 - 486		44 - 208	510 - 208	
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															1150965		573345		807509		1150960		689674	954614	
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S0040: 1, S0318: 1,	S0334: 1, S0316: 1,	S0340: 1, H0038: 1,	L0598: 1, L0800: 1 and	S0276: 1.	AR061: 2, AR089: 1	L0752: 3, L0747: 2,	H0294: 1, H0253: 1,	H0046: 1, H0040: 1,	H0063: 1, H0494: 1,	S0352: 1, L0769: 1,	L0766: 1, L0804: 1,	L0805: 1, L0791: 1,	H0521: 1, L0779: 1,	L0780: 1, L0731: 1 and	L0758: 1.	AR061: 7, AR089: 5	H0618: 12, H0253: 8,	H0038: 6, L0758: 6,	L0779: 5, H0616: 3,	F0041: 1, L0776: 1,	S0274: 1 and H0543: 1.				AR061: 0, AR089: 0
		91		94	7	*		Jacobson		,				_ 			Cys-13 to Thr-18,		Glu-61 to Pro-68,	Lys-105 to Ala-136,		Leu-163 to Gly-171,	Thr-205 to Gln-222,	Pro-251 to Gln-257.	
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					136									-		137									138
					751985		•			·	, ,	,				922923									503313
					HTLBH67											HTLJC71							÷.		HTPAD46
					126										,	127									128

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L0794: 4, H0039: 2,	S0358: 1, H0013: 1,	H0575: 1, L0770: 1,	L0769: 1 and L0749: 1.	AR089: 1, AR061: 1	H0634: 2	AR089: 4, AR061: 2	L0439: 5, S0002: 3,	L0604: 3, H0619: 2,	H0024: 2, H0625: 2,	L0768: 2, L0757: 2,	H0638: 1, S0420: 1,	S0360: 1, H0586: 1,	L0163: 1, S0214: 1,	L0143: 1, H0264: 1,	L0769: 1, L0764: 1,	L0774: 1, L0651: 1,	L0659: 1, L0542: 1,	L0789: 1, H0539: 1,	H0521: 1, S0044: 1,	L0777: 1, L0758: 1,	L0599: 1 and H0422: 1.	AR089: 1, AR061: 0	L0776: 5, L0764: 4,	L0743: 4, L0740: 3,	L0750: 3, L0777: 3,
				Thr-15 to Asp-25,	Glu-69 to Leu-89.	Gln-27 to Trp-45.				,	-			·								Gln-1 to Lys-8,	Gly-10 to Trp-17,	Val-28 to Gly-43,	Thr-54 to Glu-63.
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				2 - 337		155 - 856																1 - 453			
				139		140								ı								141			
				911390		933357												****	<u> </u>			726102			
			-	HTTKP07		HUCOW17																HWHGF52			
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L0731: 3, S0001: 2, H0438: 2, H0052: 2, H0194: 2, H0201: 2, L0526: 2, H0144: 2, L0742: 2, H0662: 1,	H0619: 1, H0261: 1, H0392: 1, H0455: 1, H0586: 1, H0587: 1, H0574: 1, H0486: 1,	H0013: 1, H0427: 1, S0010: 1, S0346: 1, T0110: 1, H0009: 1,	L0157: 1, H0320: 1, H0051: 1, T0006: 1, H0604: 1, H0163: 1,	L0638: 1, L0630: 1, L0646: 1, L0773: 1, L0651: 1, L0523: 1,	L0805: 1, L0666: 1, L0663: 1, L0664: 1, H0547: 1, H0660: 1, S0404: 1, L0744: 1,	L0439: 1, L0752: 1, S0434: 1 and L0595: 1. AR089: 1, AR061: 1
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354: 2,	517: 2,	46: 2,	53: 2,	56: 1,	57: 1,	20: 1,	41: 1,	13: 1,	56: 1,	22: 1,	71: 1,	35: 1,	00: 1,	69: 1,	64: 1,	59: 1,	30: 1,	47: 1,	90: 1,	36: 1,	48: 1,	56: 1,	57: 1,	6: 1,	10136:
L0803: 3, S0354: 2,	H0052: 2, H0617: 2,	L0770: 2, L0646: 2,	S0028: 2, L0753: 2,	H0445: 2, H0556: 1	S6024: 1, H0657: 1	S0418: 1, S0420:	H0351: 1, H0441:	H0586: 1, H0013:	S0280: 1, H0156:	L0021: 1, H0122:	S0010: 1, H0571:	L0163: 1, H0135:	H0412: 1, H0100:	L0351: 1, L0769:	L0639: 1, L0764:	L0649: 1, L0659:	L0809: 1, L0530:	H0520: 1, H0547:	H0519: 1, H0690:	H0539: 1, S0136:	H0696: 1, L0748:	L0747: 1, L0756: 1	L0779: 1, L0757: 1	S0434: 1, S0436: 1,	S0011: 1 and H0136:
0807	H0052	L0770	S0028:	H0445	S6024:	S0418:	H0351	H0586	S0280:	L0021:	S0010:	L0163:	H0412	L0351:	L0639:	L0649:	L0809:	H0520	H0519	H0539	H0696:	L0747:	L0779:	S0434:	S0011:
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Ala-70 to Tyr-77,	Arg-130 to Ser-140.									,															
Ala-70	Arg-13														-							•			
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	AR089: 5, AR061: 2	S0358: 5, L0596: 3,	L0771: 2, L0758: 2,	S0354: 1, S0376: 1,	T0109: 1, H0036: 1,	H0590: 1, L0040: 1,	H0038: 1, H0616: 1,	L0646: 1, L0764: 1,	L0768: 1, L0775: 1,	L0659: 1 and S0404: 1.			AR089: 2, AR061: 2	S0358: 6, L0794: 4,	L0758: 4, S0354: 3,	L0779: 3, L0596: 3,	S0376: 2, H0036: 2,	Н0620: 2, Н0063: 2,	L0771: 2, L0803: 2,	L0654: 2, L0659: 2,	T0109: 1, H0013: 1,	H0590: 1, H0052: 1,	H0596: 1, T0110: 1,	L0040: 1, H0090: 1,	H0038: 1, H0040: 1,
Gly-1 to Ser-7.										,	Ser-25 to Ala-52,	Phe-64 to Glu-71.	Pro-11 to Ala-35,	Phe-47 to Glu-54,	Glu-78 to Gly-83,	Gln-94 to Ser-106,	Ser-114 to Val-120.						~		
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1 - 261	695 - 333										134 - 535		3 - 539												
521	143										522		144			,									ļ
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,	HWLFH94												HWMBM13												
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H0616: 1, H0429: 1,	H0561: 1, L0646: 1,	L0764: 1, L0768: 1,	L0766: 1, L0775: 1,	L0790: 1, L0792: 1,	S0404: 1, S0390: 1,	L0777: 1, L0755: 1,	L0592: 1 and S0458: 1.	AR089: 1, AR061: 1	S0354: 16, H0457: 7,	L0758: 3, H0555: 2,	H0170: 1, H0657: 1,	H0255: 1, H0662: 1,	S0360: 1, H0036: 1,	H0150: 1, H0051: 1,	H0553: 1, L0800: 1,	L0644: 1, L0771: 1,	L0803: 1, L0787: 1,	L0663: 1, H0144: 1,	S0374: 1, H0670: 1,	H0522: 1, L0749: 1,	S0452: 1 and H0506: 1.	AR061: 1, AR089: 1	L0761: 4, L0439: 4,	L0758: 4, L0769: 3,	L0771: 3, L0662: 3,
						·		Ser-11 to Leu-17,	Pro-20 to Val-26,	Ser-87 to Lys-95,	Thr-109 to Lys-116,	Pro-164 to Gln-170,	Glu-222 to Ser-227,	Ser-292 to Gln-303,	Asp-315 to Gly-324,	Gly-326 to Ala-333.						Pro-93 to Asp-102,	Pro-112 to Ala-119,	Ser-131 to Pro-150,	Glu-188 to Gly-196.
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L0666: 3, L0665: 3, L0741: 3, L0743: 3, H0559: 2, H0318: 2, H0266: 2, L0776: 2,	L0809: 2, L0664: 2, L0740: 2, L0747: 2, L0750: 2, L0757: 2,	S0356: 1, H0587: 1, H0581: 1, H0052: 1, H0545: 1, H0086: 1,	H0620: 1, L0119: 1, H0039: 1, L0637: 1,	L0800: 1, L0764: 1,	L0657: 1, L0659: 1,	L0636: 1, L0782: 1, L0663: 1, H0520: 1,	S0044: 1, L0748: 1,	L0/54: 1, L0/79: 1, L0755: 1, L0731: 1,	L0592: 1, S0276: 1,	H0677: 1 and S0456: 1.				AR061: 3, AR089: 1
				·							Gln-19 to Glu-26,	Phe-33 to Lys-38,	Asn-45 to Val-52.	Ala-7 to Lys-19,
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H0254: 2, H0255: 2, S0045: 2, H0266: 2,	H0052: 1, H0050: 1,	H0063: 1, H0488: 1 and	H0423: 1.	-	·			AR061: 4, AR089: 2	L0777: 11, L0748: 10,	L0803: 8, L0794: 7,	L0750: 6, H0620: 5,	L0749: 5, H0622: 4,	L0805: 4, L0809: 4,	L0665: 4, H0550: 3,	H0575: 3, H0023: 3,	L0659: 3, L0790: 3,	S0356: 2, H0549: 2,	S0222: 2, H0592: 2,	H0427: 2, L0157: 2,	H0213: 2, L0763: 2,	L0662: 2, L0774: 2,	L0789: 2, L0666: 2,	H0539: 2, L0743: 2,	L0744: 2, L0600: 2,
Gly-30 to Gly-35, Ser-50 to Glu-61,	Ala-74 to Pro-81.			Pro-9 to Lys-25,	Gly-36 to Gly-41,	Ser-56 to Glu-67,	Ala-80 to Pro-87.	His-1 to Asp-11,	Val-33 to Pro-57,	Gly-68 to Glu-74,	Pro-76 to Pro-81,	Phe-93 to Val-120,	Pro-131 to Pro-146,	Pro-161 to Pro-168,	Tyr-178 to Ser-184,	Pro-187 to Gly-215,	Asn-229 to Asn-244,	Asp-250 to Trp-255,	Pro-258 to Asp-263,	Pro-300 to Val-310,	Asp-364 to Glu-371,	Thr-441 to Lys-446,	Ser-462 to Thr-477,	Lys-487 to Trp-492.
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564: 1	58: 1,	111:1	587: 1	156: 1	309: 1	545: 1	012: 1	H0051: 1, S0051: 1,	587: 1	424: 1	517; 1	1,999	100: 1	36: 1,	37: 1,	64: 1,	50: 1,	55: 1,	68: 1,	26: 1,	4: 1,	L0740: 1, L0747: 1,	58: 1,	L0759: 1, S0194: 1 and	
1, H00	1, S03	1, H0 ²	1, H0	1, HO	1, HO	1, HO	1, HO	1, S00	1, H0	1, H0	1, H0	1, S03	1, H0	I, L05	1, L06	1, L07	I, L06	1, L06	1, L03	1, S01	1, S00	I, L07	I, L07	1, S01	
S0282: 1, H0664: 1	L0005: 1, S0358: 1	S0360: 1, H0411:	H0441: 1, H0587:	S0280: 1, H0156:	H0618: 1, H0309:	H0327: 1, H0545:	H0050: 1, H0012:	3051:	3375:	H0292: 1, H0424:	Н0553: 1, Н0617;	H0124: 1, S0366:	H0616: 1, H0100:	S0210: 1, L0536: 1	L0769: 1, L0637:	L0644: 1, L0764:	L0804: 1, L0650: 1	784:	_0367: 1, L0368:	.0663: 1, S0126: 1	S0330: 1, S0044: 1	740:	752:	759:	H0352:
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						AR061: 520, AR089:	428	S0040: 1, H0669: 1,	H0662: 1, \$0420: 1,	80358: 1, 80376: 1,	H0632: 1, T0040: 1,	T0110: 1, H0633: 1,	L0800: 1, H0666: 1,	S0152: 1, S0028: 1,	L0581: 1 and L0594: 1.	AR061: 4, AR089: 3	L0748: 20, L0731: 8,	L0755: 6, H0031: 5,	H0644: 5, H0090: 5,	L0775: 5, L0749: 5,	S0360: 4, L0770: 4,	L0766: 4, L0740: 4,	L0754: 4, L0777: 4,	L0757: 4, L0758: 4,	H0050: 3, L0764: 3,
Thr-2 to Asp-9,	Val-31 to Pro-55,	Gly-66 to Glu-72,	Pro-74 to Pro-79,	Phe-91 to Val-118,	Pro-129 to Pro-144.	Gln-2 to Glu-12.				,										-					
1138						762										763									
2 - 1567						3 - 707						-		_		22 - 1137			-						
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L0768: 3, L0666: 3, L0665: 3, L0750: 3, L0756: 3, S0212: 2,	H0580: 2, H0545: 2, H0123: 2, L0471: 2,	H0012: 2, S0022: 2,	H0622: 2, H0553: 2, H0383: 2, S0344: 2,	L0662: 2, L0657: 2,	L0663: 2, L0664: 2,	H0144: 2, H0555: 2,	S0390: 2, L0743: 2,	L0747: 2, L0759: 2,	L0581: 2, L0599: 2,	H0265: 1, H0295: 1,	T0049: 1, S0358: 1,	H0619: 1, L0717: 1,	H0592: 1, H0486: 1,	L0477: 1, T0039: 1,	T0040: 1, H0013: 1,	S0010: 1, H0318: 1,	H0052: 1, H0046: 1,	H0023: 1, H0051: 1,	T0079: 1, H0355: 1,	H0510: 1, H0290: 1,	S0250: 1, H0628: 1,
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				٠.				*		,					Pro-52 to Asp-57,	Asp-67 to Trp-72,	Lys-87 to Gly-92,	Asp-98 to Gly-104.	Gly-36 to Asp-42,	Pro-51 to Ala-56,	Gln-84 to Leu-91,	His-105 to His-112,	Tyr-115 to Pro-124,	Pro-155 to Ser-162,	Cys-167 to Ala-173,
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		AR089: 81, AR061: 32	H0341: 9, H0657: 7,	S0358: 4, H0251: 4,	H0428: 4, L0748: 4,	L0750: 4, H0445: 4,	S0116: 3, H0333: 3,	H0318: 3, T0041: 3,	S0126: 3, H0670: 3,	H0648: 3, H0543: 3,	H0170: 2, S0376: 2,	S0360: 2, S0007: 2,	H0619: 2, H0393: 2,	H0486: 2, H0156: 2,	H0596: 2, H0046: 2,	H0014: 2, H0059: 2,	T0004: 2, H0647: 2,	L0521: 2, L0375: 2,	L0517: 2, H0659: 2,
His-178 to Leu-190, Ser-217 to Ala-224, Pro-226 to Gly-234, Lys-270 to Ala-275, Pro-316 to Lys-323.	Oly-10 to Ala-10, Pro-25 to Ala-30, Gln-58 to Leu-65.	Arg-13 to Gly-21,	Arg-24 to Gly-31,	Ser-41 to Gln-73,	Glu-83 to Gly-92,	Asp-98 to Ala-103,	Asn-105 to Gln-115,	Glu-129 to Glu-135,	Asp-142 to Gly-147,	Val-149 to Met-154,	His-171 to Lys-177,	Pro-187 to Gly-196,	Ala-199 to Cys-208,	Arg-230 to Tyr-245,	Glu-249 to His-256,	Asn-265 to Phe-270,	Val-277 to Arg-286,	Ala-292 to Asp-300,	Leu-327 to Pro-351,
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H0658: 2, H0660: 2,	H0672: 2, S0380: 2,	H0521: 2, S0044: 2,	H0576: 2, L0747: 2,	L0485: 2, L0595: 2,	L0362: 2, S0026: 2,	H0624: 1, S0180: 1,	S0212: 1, H0663: 1,	H0305: 1, H0459: 1,	S0418: 1, S0420: 1,	S0045: 1, S0046: 1,	H0351: 1, S0222: 1,	H0392: 1, H0249: 1,	H0643: 1, H0331: 1,	H0618: 1, T0071: 1,	H0581: 1, H0421: 1,	H0263: 1, L0040: 1,	H0546: 1, H0009: 1,	H0123: 1, H0050: 1,	L0471: 1, H0012: 1,	H0023: 1, H0015: 1,	H0083: 1, H0510: 1,	S0336: 1, H0687: 1,	H0290: 1, H0028: 1,	S0250: 1, S0022: 1,	H0615: 1, T0006: 1,
Gln-374 to His-380,	Leu-382 to Gly-391,	Lys-393 to Gly-402.					· -																		
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H0030: 1, H0169:	S0364: 1, H0068:	S0366: 1, H0376:	H0598: 1, H0090:	H0040: 1, H0412: 1	F0069: 1, L0564:	r0042: 1, H0494:	H0359: 1, H0646:	S0422: 1, H0026:	.0520: 1, L0625:	.0764: 1, L0767:	.0806: 1, L0655:	.0657: 1, L0809:	.0519: 1, L0789:	_0664: 1, S0374:	_0565: 1, H0689:	H0435: 1, H0414:	Н0666: 1, Н0539:	S0378: 1, S0004:	S0146: 1, S0027: 1	S0028: 1, S0206:	L0741: 1, L0439:	.0740: 1, L0754:	.0749: 1, L0756:	L0777: 1, L0731: 1	L0758: 1, L0581: 1
H00	803	S03	H05	H00	T000	T00	H03	S042	L052	T076)807 	5907I	L051) 	T056	H043	H066	S037	S014	S002	L074	L074	L074	L077	L075
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	L0599: 1, L0608: 1,	L0594: 1, L0603: 1,	H0668: 1, H0665: 1,	H0667: 1, S0194: 1,	H0542: 1, H0423: 1,	H0422: 1, S0424: 1 and	H0506: 1.	AR054: 41, AR050:	39, AR051: 30, AR089:	7, AR061: '5	H0618: 2, H0040: 1	and H0522: 1.			AR061: 7, AR089: 2	H0619: 1, H0575: 1,	H0615: 1 and S0028: 1.				AR089: 1, AR061: 0	\$0180: 1			AR089: 4, AR061: 3	H0657: 3, H0253: 3,
		-											Thr-27 to Asn-33,	Thr-63 to Asp-69.	Gln-93 to Arg-105,	Ser-130 to Ile-135,	Ser-166 to Lys-175,	Ser-238 to Glu-243.	Gln-93 to Arg-105,	Ser-130 to Ile-135.	Thr-45 to Phe-55,	Leu-62 to Asn-67.	Thr-41 to Phe-51,	Leu-58 to Asn-63.	Ile-8 to Arg-16,	Leu-104 to Asp-110,
								992					1141	-	191				. 1142		892		1143		692	
								81 - 623					149 - 622		1 - 774				1 - 477		3 - 416		2 - 295		2 - 580	
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Arg-133 to Leu-141,	Gly-182 to Asp-187.									,														<u> </u>	
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	Leu-20 to Pro-34, Lys-36 to Leu-55, Arg-63 to Gln-72, Pro-215 to Thr-222, Ile-288 to Leu-297, Ala-337 to Gly-346.	Ala-30 to Gly-39. Asp-60 to Lys-75, Glu-136 to Gln-142.
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S0354: 4, L0471: 4,	.0794: 4, L0653: 4,	L0809: 4, L0666: 4,	.0748: 4, H0441: 3,	H0051: 3, H0266: 3,	S0003: 3, H0644: 3,	H0032: 3, L0770: 3,	L0803: 3, L0664: 3,	H0658: 3, S0380: 3,	S3014: 3, S0206: 3,	L0754: 3, L0750: 3,	0192	H0657: 2, S0298: 2,	S0358: 2, S0360: 2,	L0717: 2, S6016: 2,	H0574: 2, T0040: 2,	H0013: 2, H0052: 2,	H0009: 2, S6028: 2,	H0428: 2, H0090: 2,	H0591: 2, S0422: 2,	L0804: 2, L0659: 2,	L0663: 2, L0665: 2,	H0144: 2, H0689: 2,	H0521: 2, S3012: 2,	S0037: 2, S0028: 2,	L0742: 2, L0745: 2,
: 4, L	1. 4, L	1,4,	. 4, F	I: 3, F	: 3, H	2: 3, I	: 3, L	3: 3, S	3, S	F 3, I	: 3, S	7: 2, S	: 2, S	': 2, S	t: 2, 1	3: 2, F): 2, S	3: 2, F	I: 2, S	F. 2, L	: 2, L	1: 2, F	I: 2, S	: 2, S	2, 1
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Thr-32 to Phe-42,	Leu-49 to Asn-54.	Glu-33 to Arg-47,	Glu-75 to Phe-87,	Tyr-167 to Lys-173,	Pro-199 to Ala-204,	Arg-249 to Lys-256,	Leu-319 to Asn-324,	Pro-385 to Glu-390,	Val-441 to Val-448,	Asn-512 to Ile-517.										Ala-4 to Phe-11,	Pro-28 to Arg-35,	Ala-49 to Lys-57,	Asp-62 to Cys-67.	Phe-4 to Arg-13,	Arg-20 to Pro-27,
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L0777: 11, H0265: 7,	L0769: 7, L0747: 5,	H0052: 4, L0764: 4,	L0438: 4, L0741: 4,	L0604: 4, S0358: 3,	H0266: 3, H0424: 3,	S0344: 3, L0775: 3,	L0776: 3, L0758: 3,	S0212: 2, H0402: 2,	S0007: 2, S0046: 2,	S0132: 2, S0222: 2,	H0253: 2, S0051: 2,	H0594: 2, H0328: 2,	H0213: 2, H0617: 2,	H0674: 2, H0412: 2,	H0100: 2, H0647: 2,	S0002: 2, L0761: 2,	L0774: 2, L0809: 2,	S0152: 2, L0742: 2,	L0439: 2, L0755: 2,	L0757: 2, H0445: 2,	L0594: 2, H0542: 2,	H0543: 2, H0484: 1,	H0254: 1, H0255: 1,	H0125: 1, S0418: 1,	S0360: 1, H0580: 1,
Thr-29 to Ala-38,	Asp-48 to Thr-54,	Ala-68 to Glu-78,	Ser-101 to Ile-108,	Asp-117 to Gln-162,	Thr-206 to Trp-212,	Cys-285 to Lys-300,	Gly-311 to Gly-316,	Thr-362 to Thr-367,	Arg-376 to Ser-382,	Pro-413 to Pro-418,	Ser-430 to Gly-435,	Asp-484 to Ser-489.									-				
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					-							Tyr-7 to Tyr-15,	Pro-43 to Ala-52,	Gln-57 to Ala-62,	Asn-68 to Ala-73,	Tyr-75 to Met-83,	Glu-115 to Leu-140,	Ala-144 to Glu-156,	Val-159 to Ser-166,	Arg-178 to Pro-186,	Arg-191 to Ile-198.				
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	Tyr-7 to Tyr-15,	Pro-43 to Ala-52,	Gln-57 to Ala-62,	Asn-68 to Ala-73,	Tyr-75 to Met-83,	Glu-115 to Leu-140,	Ala-144 to Glu-156,	Val-159 to Ser-166,	Arg-178 to Pro-186,	Arg-191 to Ile-198.					Ala-54 to Ile-59,	His-71 to His-82.	Met-5 to Asn-11,	Gly-20 to Arg-30,	Thr-36 to Ile-41,	His-136 to Thr-143, S	Thr-152 to Asp-161,
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Gly-176 to Cys-183.	Arg-1 to Lys-11,	Gly-70 to Ala-76,	Lys-118 to Thr-125,	Pro-161 to His-168,	Arg-170 to Lys-175,	Glu-222 to Leu-228,	Pro-259 to Gly-265,	Asn-299 to Leu-305,	Leu-309 to Gly-314,	Pro-316 to Ser-327.	Asn-1 to Lys-10,	Thr-22 to Arg-27,	Gly-69 to Ala-75.	Glu-7 to Tyr-14,	Arg-21 to Leu-29,	Pro-42 to Ala-54,	Arg-95 to Phe-106.			Glu-7 to Tyr-14,	Arg-21 to Lys-30.	Asn-54 to Asn-63,
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	208965										929762			1185273				*		818806		1105672
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H0305: 1		AR089: 6, AR061: 3	H0497: 1, H0617: 1,	L0769: 1, L0766: 1,	L0775: 1, H0670: 1 and	H0672: 1.		AR061: 3, AR089: 2	L0748: 8, H0212: 3,	S0010: 2, L0438: 2,	L0752: 2, H0170: 1,	H0052: 1, H0596: 1,	H0051: 1, H0032: 1,	H0068: 1, L0800: 1,	L0764: 1, L0803: 1,	L0791: 1, H0521: 1,	L0749: 1, L0758: 1,	L0599: 1 and S0192: 1.						AR089: 2, AR061: 0] S0045: 1 and S0053: 1. $]$
Gln-70 to Glu-75.	Lys-19 to Thr-26.	Asp-1 to Lys-12,	Pro-18 to Arg-26,	Asp-51 to Val-74,	Ala-80 to Leu-102.			Glu-25 to Ser-30,	Glu-57 to Thr-62,	His-64 to Ser-72,	His-101 to Pro-106,	Val-111 to Gln-117.							Tyr-7 to Tyr-15,	Pro-43 to Ala-52,	Gln-57 to Ala-62,	Asn-68 to Ala-73,	Tyr-75 to Met-83.	Gln-38 to Ser-51.	
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	50 - 364	68 - 913					68 - 460	541 - 146		. *									505 - 185					287 - 3	
	542	691					543	170											544					171	
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	AR089: 3, AR061: 2	H0457: 8, H0264: 2,	H0645: 1, H0549: 1,	H0069: 1, H0599: 1,	H0318: 1, H0566: 1,	H0132: 1, H0658: 1 and	S0350: 1.			-									AR089: 0, AR061: 0	T0010: 2	AR089: 14, AR061: 5	H0545: 1, H0560: 1	and L0805: 1.		
Gln-38 to Ser-51.	Pro-1 to Gin-8,	Lys-32 to Lys-45,	Pro-51 to Arg-59,	Asp-84 to Val-107,	Ala-113 to Leu-135,	Gln-137 to Leu-156,	Gln-160 to Arg-170,	Gln-182 to Pro-194,	Lys-201 to Ser-213,	Arg-272 to Tyr-278.	Pro-1 to Gln-8,	Lys-32 to Lys-45,	Pro-51 to Arg-59,	Asp-84 to Val-107,	Ala-113 to Leu-135,	Gln-137 to Leu-156,	Gln-160 to Arg-170,	Gln-182 to Leu-198.			Ala-11 to Asn-16,	Ala-18 to Leu-25,	Lys-40 to Arg-52,	Tyr-58 to Ile-76,	Lys-151 to Thr-162,
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		AR061: 4, AR089: 3	H0521: 4, H0265: 1,	H0341: 1, S0212: 1,	S0418: 1, S0356: 1,	H0619: 1, T0114: 1,	10004: 1, T0048: 1,	H0052: 1, H0081: 1,	H0024: 1, H0124: 1,	H0040: 1, H0551: 1,	H0477: 1, H0623: 1,	H0059: 1, H0494: 1,	H0641: 1, S0144: 1,	S0126: 1, H0660: 1,	H0672: 1, L0743: 1 and	H0445: 1.								
Gln-176 to Gly-182.	Ser-11 to Ala-21, Asp-23 to Ile-28			Joseph Land	51			1	,					`		·	Met-16 to Ala-23,	Ile-34 to Arg-41,	Lys-48 to Pro-54,	Leu-65 to Thr-82,	Glu-104 to Thr-110,	Arg-119 to Tyr-126,	Gly-135 to Ala-144,	His-153 to His-158,
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	AR061: 153, AR089: 48 L0599: 12, L0766: 11, L0754: 8, L0803: 2, L0731: 2, H0624: 1, H0171: 1, S0040: 1, H0650: 1, S0298: 1, S0282: 1, H0580: 1, S046: 1, S0222: 1, H0486: 1, S0010: 1, H0318: 1, S0010: 1, H0318: 1,	H0581: 1, H0309: 1, H0416: 1, T0006: 1, H0063: 1, T0041: 1, H0560: 1, S0422: 1, S0002: 1, L0641: 1, L0363: 1, L0523: 1, L0659: 1, H0547: 1, H0539: 1, S0152: 1,
Asn-178 to Gln-194, Arg-197 to His-202, Ser-236 to Arg-241, Gln-245 to Arg-250.	Ala-15 to Gln-22, Pro-55 to Val-91, Glu-116 to Tyr-122, His-130 to His-135, Asn-155 to Tyr-162, Leu-164 to Cys-186, Ser-213 to Gln-222, Ser-228 to Gly-239, Ile-281 to Glu-286, Lys-296 to Lys-303, Val-310 to Glu-315, Thr-320 to Asp-335, Arg-344 to Ala-352.	
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S0242: 1, H0543: 1 and H0423: 1.				AR089: 1, AR061: 0	H0038: 2	AR061: 5, AR089: 2	H0038: 3, H0575: 1,	H0052: 1, H0628: 1,	H0412: 1, L0780: 1 and	L0758: 1.		AR061: 5, AR089: 5	H0253: 4, H0618: 3,	L0758: 3, L0779: 2 and	L0794: 1.					AR089: 19, AR061: 8	L0747: 5, L0731: 2,	H0656: 1, H0351: 1,	Н0392: 1, Н0333: 1,	S0362: 1, S0306: 1,
	Cys-3 to Glu-8,	Gly-13 to Gln-19,	Pro-52 to Val-88.	Ala-15 to Tyr-24,	His-32 to Asp-39.	Gln-85 to Gly-91,	Ser-99 to Arg-104.									Arg-1 to Arg-6,	Ala-49 to Tyr-58,	Pro-67 to Lys-80,	Ser-92 to Trp-108.	Ala-6 to Tyr-17.				
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			Asp-52 to Leu-57, Lys-82 to Thr-87,	Ser-90 to Trp-98, Ser-118 to Leu-123.	·.			Lys-14 to Glu-27.
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8: 5, L	7: 4, L	H: 3, E	7: 3, L	0: 3, L	3: 2, H	6: 2, H	0: 2, L	3: 2, L	2: 2, S.	7: 2, L	9: 2, H	S6024: 1, L0002:	H0657: 1, H0341:	S0358: 1, S0360: 1	S0132: 1, L0717:	2: 1, H	9: 1, S	5: 1, H(1: 1, To	H0544: 1, L0471: 1	H0014: 1, S0362:	H0083: 1, H0188:	H0428: 1, H0646:	H0538: 1, L0598:	1.0762: 1.1.0763: 1
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										,				Phe-22 to Ala-37,	Cys-94 to Asn-100,	Gly-137 to Pro-145,	Glu-172 to Ala-179,	Ile-217 to Asp-222.							
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S0002: 2, H0144: 2,	L0438:	L0744:	L0595: 2, L0601: 2,	10665:	H0556: 1, H0222: 1	H0294: 1, H0583: 1	H0650: 1, H0657:	H0484: 1, H0306:	S0418: 1, S0420: 1	S0354: 1, H0580:	S0007: 1, S0046:	H0619: 1, H0550:	H0392: 1, H0586:	H0333: 1, H0486:	Н0122: 1, Н0196:	H0597: 1, H0544:	H0009: 1, H0172:	L0471: 1, H0023:	H0071: 1, H0266:	H0290: 1, H0553:	H0628: 1, H0551:	H0056: 1, H0623:	S0038: 1, H0494:	H0625: 1, H0561:	H0386: 1, H0509:
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,							<u> </u>					T .		1		Leu-50 to Asp-61,	Ser-100 to Leu-107, 6	Ala-120 to Thr-130.		Gly-15 to Thr-21, △	Glu-76 to Lys-86.			<u></u>	S
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AR089: 16, AR061: 8	S0038: 2, H0438: 1,	S0049: 1 and H0547: 1.	AR061: 8, AR089: 3	S0222: 1, H0052: 1,	H0194: 1, H0290: 1 and	H0264: 1.	H0052: 1 and L0471:	1.	AR061: 2, AR089: 2	S0358: 1, H0413: 1,	L0502: 1, L0657: 1,	H0522: 1 and H0422: 1.	AR089: 14, AR061: 7	H0341: 1 and H0422:	<u> </u>	,			AR089: 25, AR061: 11 5q34	L0601: 5, H0266: 4,	S0222: 3, H0265: 2,	H0556: 2, H0575: 2,	H0052: 2, H0271: 2,	S0114: 1, S0134: 1,	S0420: 1, H0393: 1,
Gln-3 to Ser-12,	Arg-33 to Arg-50,	Ser-93 to Glu-98.	Asn-6 to Pro-13.	¥	8		Thr-2 to Gln-7.		Lys-15 to Ser-20,	Arg-51 to Arg-60,	Lys-64 to Pro-101.		Leu-1 to Glu-9,	Gln-43 to Ala-52,	Gly-169 to Gly-176,	Arg-178 to Leu-185,	Pro-192 to Phe-199.	Arg-1 to Glu-8.	Asp-90 to Lys-105.	-					
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H0550: 1, H0497: 1,	H0318: 1, H0581: 1,	H0251: 1, T0115: 1,	H0014: 1, H0286: 1,	H0494: 1, H0561: 1,	L0766: 1, L0657: 1,	H0698: 1, H0684: 1,	S0330: 1, H0521: 1,	S3014: 1, L0777: 1,	S0260: 1, L0591: 1,	L0594: 1 and H0543: 1.	AR089: 4, AR061: 0	H0581: 1, H0494: 1,	H0521: 1, H0543: 1 and	L0465: 1.	AR089: 1, AR061: 1	H0522: 2 and L0766:	1.	AR061: 2, AR089: 2	L0759: 12, L0439: 11,	L0766: 7, L0775: 5,	H0521: 5, L0755: 5,	L0748: 4, L0756: 4,	L0777: 4, L0731: 4,	L0581: 4, L0619: 3,	L0666: 3, L0779: 3,
					-						Ala-13 to Asn-20,	Phe-38 to Gly-46,	Glu-89 to His-95.		Val-2 to Gly-8,	Asp-20 to Gln-26.		Pro-26 to Leu-34,	His-42 to Asn-51.						
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L0757: 3, L0588: 3	S0418: 2, L0618: 2,	H0580: 2, L0055: 2,	.0769: 2, L0773: 2,	.0774: 2, L0791: 2,	L0747: 2, L0750: 2,	H0265: 1, H0663: 1	S0356: 1, H0208:	Н0370: 1, Н0108:	H0575: 1, H0618:	H0544: 1, H0545:	S0050: 1, H0510:	H0286: 1, H0031:	H0644: 1, H0068:	H0135: 1, L0564:	H0494: 1, L0475:	H0396: 1, S0144:	S0002: 1, S0426:	.0763: 1, L0761:	_0642: 1, L0764:		.0806: 1, L0661:		_0663: 1, H0519:	H0435: 1, H0658: 1	S3014: 1, L0751:
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		Met-7 to Ser-12,	Ser-20 to Arg-30,	Asp-85 to Ala-92,	Met-119 to Asn-146,	Pro-151 to Asp-161.		Phe-73 to Pro-81,	His-156 to Asp-165,	Pro-182 to Lys-187,	Lys-196 to Asp-201,	Pro-204 to Leu-214,	Pro-224 to Asp-231.												
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H0544: 1, H0545: 1, S0050: 1, H0510: 1, H0286: 1, H0031: 1, H0644: 1, L0564: 1, H0135: 1, L0564: 1, H0396: 1, S0144: 1, S0002: 1, S0426: 1, L0763: 1, L0761: 1, L0662: 1, L0768: 1, L0662: 1, L0768: 1, L0663: 1, H0519: 1, H0435: 1, H0558: 1, S3014: 1, L0751: 1, L0749: 1, L0603: 1, H0665: 1 and H0542: 1.		AR089: 8, AR061: 2 S0218: 1 and H0486: 1.	AR061: 9, AR089: 4 H0624: 1
	Pro-14 to Ala-20, Pro-51 to Leu-59, His-67 to Thr-77.	His-130 to Lys-140.	Leu-10 to Gly-16, Pro-37 to Glu-45, Glu-78 to Cys-87.
	1166	813	814
	2 - 538	3 - 464	2 - 796
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AR061: 2, AR089: 1 H0013: 1 and S0027: 1.	AR061: 1, AR089: 1 L0774: 2 and H0144: 2.	AR061: 8, AR089: 4 L0547: 2, S0046: 1, L0471: 1, L0772: 1, L0529: 1 and L0780: 1.	AR061: 4, AR089: 2 H0046: 1 and L0758: 1.	AR089: 1, AR061: 1 L0748: 5, S0242: 3, H0615: 2, S0376: 1, S0360: 1, L0717: 1, L0641: 1, L0766: 1, L0664: 1, H0478: 1, L0593: 1 and S0196: 1.	AR089: 0, AR061: 0 H0620: 2, L0761: 2, L0766: 2, L0744: 2, L0754: 2, L0596: 2, H0686: 1, H0295: 1, H0657: 1, H0597: 1, H0009: 1, H0264: 1,
	Phe-8 to Lys-27, Ser-79 to Ser-87, Cys-102 to Val-116.	-		Cys-1 to Val-10, Ala-14 to Met-22.	Asp-2 to Pro-7, Pro-15 to Gln-20.
815	816	817	818	819	820
111 - 455	362 - 871	1 - 351	3 - 416.	2 - 775	1 - 300
202	203	204	205	206	207
960914	974353	939957	909762	909758	934019
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S0002: 1, L0769: 1,	L0774: 1, L0805: 1,	L0657: 1, L0790: 1,	H0690: 1 and H0521: 1.	AR089: 2, AR061: 1	S0360: 1, H0013: 1,	L0664: 1 and H0542: 1.	AR089: 3, AR061: 2	L0748: 8, H0039: 5,	H0622: 5, L0664: 5,	L0439: 5, L0779: 5,	L0731: 5, L0758: 5,	L0665: 4, L0744: 4,	L0601: 4, H0667: 4,	H0255: 3, H0618: 3,	L0666: 3, L0438: 3,	S0126: 3, L0602: 3,	L0742: 3, L0604: 3,	L0595: 3, H0542: 3,	H0265: 2, S0358: 2,	H0393: 2, S0278: 2,	H0550: 2, H0333: 2,	H0599: 2, H0318: 2,	H0545: 2, H0123: 2,	H0050: 2, H0620: 2,	H0179: 2, H0271: 2,
							Gly-59 to Ser-68,	Ala-87 to Glu-98,	Pro-106 to Asn-121,	Ser-148 to Lys-159,	Phe-207 to Ala-222,	He-284 to Lys-289.	-												
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S0036: 2, H0135: 2,	H0634: 2, H0087: 2,	H0100: 2, H0633: 2,	S0210: 2, S0002: 2,	L0769: 2, L0646: 2,	L0768: 2, L0774: 2,	H0144: 2, L0565: 2,	H0689: 2, S0027: 2,	L0747: 2, L0755: 2,	L0593: 2, H0665: 2,	H0556: 1, T0002: 1,	H0222: 1, H0685: 1,	H0294: 1, S0430: 1,	H0583: 1, H0650: 1,	H0657: 1, S0212: 1,	S0282: 1, H0484: 1,	H0306: 1, S0418: 1,	S0420: 1, S0354: 1,	S0360: 1, H0580: 1,	S0007: 1, S0046: 1,	H0619: 1, H0351: 1,	H0549: 1, H0392: 1,	H0586: 1, H0486: 1,	T0060: 1, L0022: 1,	H0122: 1, H0196: 1,	H0597: 1, H0544: 1,
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H0009: 1, H0172: 1,	L0471: 1, H0023: 1,	H0071: 1, H0266: 1,	H0290: 1, S0022: 1,	H0030: 1, H0553: 1,	H0628: 1, H0182: 1,	H0617: 1, H0606: 1,	H0551: 1, H0413: 1,	H0056: 1, H0623: 1,	S0038: 1, H0494: 1,	H0625: 1, H0561: 1,	H0386: 1, H0509: 1,	H0131: 1, H0130: 1,	H0646: 1, S0144: 1,	S0344: 1, S0426: 1,	H0529: 1, L0763: 1,	L0770: 1, L0637: 1,	L0372: 1, L0662: 1,	L0775: 1, L0776: 1,	L0659: 1, L0383: 1,	L0790. 1, H0547. 1,	H0435: 1, H0658: 1,	H0670: 1, S0330: 1,	H0521: 1, H0436: 1,	S0390: 1, S0028: 1,	S0032: 1, L0750: 1,
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L0753: 1, L0757: 1,	L0759: 1, S0260: 1,	H0445: 1, H0595: 1,	L0597: 1, L0366: 1,	H0668: 1, S0242: 1,	H0423: 1, H0422: 1 and	H0352: 1.	AR089: 3, AR061: 2	H0597: 1, H0435: 1	and H0543: 1.		AR089: 2, AR061: 2	L0789: 4, L0758: 4,	H0657: 3, H0052: 3,	H0046: 3, L0438: 3,	L0744: 3, L0779: 3,	L0005: 2, H0586: 2,	H0581: 2, H0194: 2,	H0038: 2, L0800: 2,	L0659: 2, H0521: 2,	L0743: 2, L0439: 2,	H0556: 1, S0282: 1,	S0358: 1, H0619: 1,	H0618: 1, H0231: 1,	H0569: 1, S0362: 1,	H0622: 1, T0006: 1,
							Ser-3 to Thr-11,	Lys-32 to Gly-39,	Thr-50 to Glu-57,	Thr-83 to Gln-88.	Gly-33 to Ser-48.														
							823				824							,					•		
							88 - 474				130 - 843														
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H0135: 1, H0616: 1,	H0413: 1, H0623: 1,	L0351: 1, S0150: 1,	L0769: 1, L0372: 1,	L0662: 1, L0794: 1,	L0775: 1, L0651: 1,	L0527: 1, L0657: 1,	L0666: 1, H0144: 1,	H0547: 1, H0690: 1,	H0658: 1, H0672: 1,	H0539: 1, S0378: 1,	H0555: 1, L0754: 1,	L0747: 1, L0780: 1,	L0596: 1, S0192: 1,	H0542: 1 and H0423: 1.	AR089: 1, AR061: 1	L0794: 4, L0438: 4,	L0761: 3, L0766: 3,	L0748: 3, L0439: 3,	H0556: 2, L0602: 2,	L0754: 2, L0779: 2,	H0580: 1, H0208: 1,	H0013: 1, T0082: 1,	S0010: 1, H0428: 1,	H0553: 1, H0038: 1,	H0616: 1 H0404: 1
										,					Gly-25 to Gln-31,	Asn-58 to Leu-63,	Lys-71 to His-76,	lle-82 to Arg-88,	Ala-134 to Thr-139.						
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L0796: 1, L0800: 1,	L0773: 1, L0533: 1,	L0803: 1, L0776: 1,	L0657: 1, L0791: 1,	H0520: 1, H0519: 1,	H0521: 1, H0187: 1,	L0731: 1, S0031: 1 and	L0366: 1.	AR089: 1, AR061: 1	L0439: 3, L0438: 2,	S0028: 2, H0656: 1,	H0645: 1, H0369: 1,	S0222: 1, S0346: 1,	H0328: 1, H0029: 1,	H0644: 1, H0169: 1,	H0591: 1, H0646: 1,	H0520: 1, H0539: 1,	L0746: 1 and L0366: 1.	AR054: 16, AR051:	15, AR050: 12, AR089:	0, AR061: 0	L0777: 6, L0758: 5,	L0779: 4, L0803: 3,	S0358: 2, H0004: 2,	L0662: 2, L0775: 2,	H0144: 2, S0126: 2,
																		Thr-15 to Arg-22,	Ala-38 to Met-43,	Gln-49 to Lys-64,	Thr-97 to Gln-108,	Thr-131 to Lys-137.			
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								919354										934483							
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S0328: 2, S3014: 2,	S0027: 2, L0743: 2,	L0748: 2, H0265: 1,	H0656: 1, S0212: 1,	H0663: 1, H0638: 1,	H0580: 1, H0632: 1,	H0486: 1, H0599: 1,	H0618: 1, L0105: 1,	H0251: 1, H0309: 1,	H0544: 1, H0123: 1,	H0050: 1, L0471: 1,	H0024: 1, H0399: 1,	S0003: 1, H0364: 1,	H0553: 1, H0038: 1,	H0412: 1, H0413: 1,	T0041: 1, S0344: 1,	S0002: 1, L0598: 1,	H0529: 1, L0645: 1,	L0363: 1, L0649: 1,	L0804: 1, L0805: 1,	L0558: 1, L0659: 1,	L0528: 1, L0789: 1,	L0792: 1, L0666: 1,	S0374: 1, H0555: 1,	S3012: 1, S0028: 1,	S0206: 1, S0032: 1,
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L0439: 1, L0757: 1, S0031: 1, H0707: 1, S0192: 1, H0423: 1, S0042: 1 and H0008: 1.	AR061: 24, AR089: 14 L0806: 3, L0772: 2, L0648: 2, H0255: 1, L0717: 1, H0586: 1, H0599: 1, H0618: 1, H0581: 1, H0052: 1, H0123: 1, L0629: 1, L0659: 1, L0663: 1, S0330: 1, H0518: 1 and	AR061: 3, AR089: 2 L0750: 4, H0519: 3, L0666: 2, L0565: 2, H0539: 2, L0742: 2, L0744: 2, L0754: 2, L0777: 2, L0759: 2, H0662: 1, S0045: 1, H0673: 1, H0251: 1, H0030: 1, H0628: 1, H0674: 1, H0529: 1, L0770: 1, L0764: 1,
	Pro-23 to Lys-28, Gln-39 to Thr-51, Lys-93 to Ala-106, Gln-112 to Pro-129, Pro-132 to Pro-143.	
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L0787: 1, H0547: 1,	H0521: 1, H0696: 1,	H0555: 1, L0747: 1,	L0749: 1, L0786: 1,	L0779: 1, L0780: 1,	L0752: 1 and L0592: 1.	AR089: 2, AR061: 2	H0519: 2, S0420: 1,	T0114: 1, H0013: 1,	S0346: 1, H0038: 1,	S0142: 1, H0520: 1,	H0521: 1 and H0136: 1.	AR089: 0, AR061: 0	H0520: 1		AR089: 1, AR061: 1	S0007: 1, S0222: 1,	S0049: 1, L0438: 1,	H0520: 1 and L0439: 1.	AR054: 34, AR051:	29, AR050: 23, AR089:	4, AR061: 4	H0615: 1	AR061: 1, AR089: 0	S0040: 1, H0580: 1,	S0222: 1, H0355: 1,
		·								,		Pro-1 to Glu-6,	His-17 to Lys-22,	Pro-52 to Gln-58.	Ala-2 to Gln-9,	Arg-22 to Val-29,	Glu-51 to Leu-64.		His-8 to Gly-18,	Glu-150 to Leu-167.			Tyr-83 to Ser-92,	Leu-118 to Tyr-123,	Leu-137 to Ser-143,
						830						831			832			-,	833				834		
						182 - 586						2 - 688			2 - 658		٠.		14 - 544			-	629 - 2161		,
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						934522						757184			909942				974911				1216683		
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S0250: 1, L0565: 1 and S0152: 1.		AR089: 0, AR061: 0	•	AR089: 3, AR061: 2	L0803: 4, L0758: 3,	80212: 2, 80358: 2,	H0038: 2, L0770: 2,	L0767: 2, L0766: 2,	L0748: 2, L0751: 2,	L0747: 2, L0759: 2,	L0588: 2, L0599: 2,	H0411: 1, H0392: 1,	H0333: 1, L0021: 1,	H0118: 1, T0115: 1,	L0471: 1, L0163: 1,	H0633: 1, L0769: 1,	L0764: 1, L0775: 1,	L0376: 1, L0806: 1,	L0805: 1, L0807: 1,	L0787: 1, H0547: 1,	S0122: 1, H0555: 1,	H0478: 1, L0744: 1,	L0740: 1, L0749: 1,	L0750: 1, L0755: 1 and
Gln-148 to Ser-158.	Gly-1 to Trp-6.	Thr-1 to Leu-12.	•	Gln-15 to Gln-21.			•		,								,							
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L0595: 1.	AR089: 14, AR061: 6	H0555: 1 and L0777:		AR061: 1, AR089: 1	S0222: 3, H0052: 3,	_0361: 3, H0179: 2,	_0769: 2, H0521: 2,	H0555: 2, L0779: 2,	.0758: 2, H0663: 1,	H0549: 1, S0220: 1,	H0586: 1, H0156: 1,	S0010: 1, H0596: 1,	S0051: 1, T0010: 1,	H0271: 1, L0143: 1,	H0617: 1, H0652: 1,	L0764: 1, L0794: 1,	L0806: 1, L0809: 1,	H0518: 1, H0478: 1,	L0751: 1, L0747: 1,	_0750: 1, L0780: 1,	L0731: 1 and L0366: 1.	AR089: 12, AR061: 4	H0598: 1 and H0135:		AR061: 2, AR089: 1
	Lys-1 to Leu-6,	Asp-25 to Pro-30.		His-9 to Ile-15.						,	4					`				, man		Lys-49 to Lys-54,	Trp-106 to Lys-112,	Leu-130 to Gly-141.	Ser-1 to Asp-7,
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	717358			942527											,							942673		,	823869
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H0370: 2, S0002: 1,	S0428: 1 and S0027: 1.	AR061: 4, AR089: 3	L0439: 6, L0777: 6,	H0052: 4, L0748: 4,	H0634: 3, L0662: 3,	L0805: 3, L0659: 3,	L0438: 3, H0547: 3,	L0750: 3, L0758: 3,	H0208: 2, H0123: 2,	H0014: 2, H0617: 2,	H0135: 2, L0769: 2,	L0766: 2, L0803: 2,	L0776: 2, L0666: 2,	L0751: 2, L0745: 2,	L0731: 2, H0265: 1,	S0408: 1, H0549: 1,	H0497: 1, L0622: 1,	H0581: 1, H0194: 1,	L0738: 1, H0546: 1,	H0024: 1, S0362: 1,	L0163: 1, T0010: 1,	H0083: 1, H0510: 1,	H0266: 1, H0428: 1,	H0622: 1, H0673: 1,	H0598: 1, S0036: 1,
Leu-38 to Ser-44,	Pro-85 to Tyr-90.	Glu-29 to Arg-35,	Arg-50 to Leu-55,	Leu-60 to Ser-69,	Lys-102 to Asp-108,	Pro-133 to Gln-141.						,											-		
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H0163: 1, H0413: 1,	L0370: 1, T0041: 1,	H0647: 1, L0637: 1,	L0667: 1, L0772: 1,	L0646: 1, L0800: 1,	L0764: 1, L0649: 1,	L0657: 1, L0809: 1,	L0788: 1, L0663: 1,	S0374: 1, H0520: 1,	H0670: 1, H0666: 1,	S0330: 1, H0539: 1,	H0521: 1, H0696: 1,	H0478: 1, S0028: 1,	L0741: 1, L0747: 1,	L0749: 1, L0780: 1,	L0752: 1 and H0543: 1.	AR061: 8, AR089: 3	L0758: 3, H0159: 2,	S0001: 1, H0618: 1,	H0660: 1 and L0779: 1.		AR089: 1, AR061: 0	H0038: 2, L0745: 2	and H0616: 1.	AR089: 15, AR061: 9	L0766: 4, L0745: 3,
		-				,				,						Glu-1 to Ala-15,	Lys-25 to Ser-32,	Asp-45 to Thr-51,	Pro-59 to Pro-65,	Pro-78 to Ser-85.	Pro-12 to Tyr-21.				
					•											842					843			844	,
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L0752: 3, S0360: 2,	L0748: 2, L0746: 2,	L0755: 2, H0624: 1,	S0114: 1, H0098: 1,	L0471: 1, H0083: 1,	H0428: 1, L0483: 1,	H0090: 1, H0616: 1,	H0494: 1, H0560: 1,	H0509: 1, L0761: 1,	L0772: 1, L0803: 1,	L0776: 1, L0655: 1,	L0792: 1, L0664: 1,	S0374: 1, L0438: 1,	H0520: 1, H0519: 1,	H0435: 1, H0648: 1,	S0152: 1, H0521: 1,	H0478. 1, L0747: 1,	L0756: 1, L0779: 1,	L0758: 1, L0759: 1,	H0667: 1, H0543: 1 and	L0465: 1.	AR061: 7, AR089: 5	H0616: 1			
									,				-								Ala-1 to Gln-7,	Lys-24 to Ser-30,	Pro-44 to Asn-53,	Glu-104 to Asp-112,	Leu-152 to Ser-157.
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AR089: 13, AR061: 13	L0666: 3, L0758: 3,	H0616: 2, L0779: 2,	S0036: 1, L0598: 1,	L0766: 1, L0651: 1,	L0806: 1, L0776: 1,	H0144: 1, H0547: 1,	H0672: 1 and H0555: 1.	AR061: 5, AR089: 1	H0616: 1 and L0758:			AR061: 7, AR089: 4	H0551: 3, H0529: 3,	L0769: 3, L0758: 3,	S0418: 2, L0770: 2,	L0773: 2, L0521: 2,	H0701: 2, S0126: 2,	L0747: 2, L0731: 2,	L0759: 2, L0589: 2,	L0601: 2, H0624: 1,	H0149: 1, H0556: 1,	H0295: 1, S0134: 1,	H0583: 1, H0661: 1,	H0592: 1, H0013: 1,	H0635: 1, H0581: 1,
Asp-22 to Asp-28,	Leu-98 to Trp-103,	Glu-123 to Trp-154.						Ile-39 to Ser-46,	Val-69 to Gln-75,	Phe-90 to Ser-100.	Ser-38 to Pro-45.	His-12 to Arg-20,	Pro-26 to Asp-43,	Ala-62 to Glu-70,	Arg-78 to Arg-83,	Phe-100 to Gln-105,	Gly-129 to Glu-136,	Met-182 to Gly-190,	Tyr-277 to Ala-284.						
846	<u>.</u>							847			1168	848		,				,				-	٠		
1 - 711								861 - 175			1 - 318	62 - 976		-									-	0	
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S0250: 1, H0212: 1, H0412: 1, S0144: 1,	L0764: 1, L0645: 1, L0764: 1, L0794: 1,	L0766: 1, L0775: 1,	L0783: 1, L0665: 1,	H0519: 1, H0435: 1,	H0672: 1, H0436: 1,	S3014: 1, S0028: 1,	L0750: 1, L0777: 1,	L0366: 1, H0667: 1 and	H0423: 1.	,						AR061: 3, AR089: 1	H0618: 3 and H0253:	Τ.		AR061: 0, AR089: 0	H0618: 64, H0253: 52,	L0758: 6, L0779: 2,	H0392: 1, H0038: 1,
										His-12 to Arg-20,	Pro-26 to Asp-43,	Ala-62 to Glu-70,	Arg-78 to Arg-83,	Phe-100 to Gln-105,	Gly-129 to Glu-136.		Phe-86 to Ala-94,	Lys-111 to Arg-118,	His-193 to Tyr-198.	Pro-3 to Gly-8,	Val-21 to Gly-30,	Gly-68 to Ala-85,	His-94 to Gly-99,
										1169						849				850			
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L0761: 1, L0803: 1,	L0806: 1 and L0697: 1.								AR089: 1, AR061:	L0766: 2, H0264: 1		AR061: 2, AR089:	L0439: 6, L0777: 6,	H0052: 4, L0748: 4,	H0634: 3, L0662: 3,	L0805: 3, L0659: 3,	L0438: 3, H0547: 3	L0750: 3, L0758: 3,	H0208: 2, H0123: 2,	H0014: 2, H0617: 2,	H0135: 2, L0769: 2,	.0766: 2, L0803: 2,	L0776: 2, L0666: 2,	L0751: 2, L0745: 2,	65: 1
ı, L08	and								1, A	2, H(and H0521: 1.	2, A	6, L0	t, L07	3, LO6	, L06	, H05	, L07	, H0	, H06	; L07	, L08	, L06	, L07	L0731: 2, H0265: 1
761:	806:								.089:)766:	H05	061:)439:	052: 4	534: 3	305: 3	138: 3	50: 3	208: 2)14: 2	135: 2	66: 2	76: 2	51:2	31: 2
<u> </u>	<u> </u>								AR	<u> </u>	and	AR	<u> </u>	HO	HO	<u>20</u>	L04	1.07	H0;)OH	H0	L07	L07	L07	L07
110,	.138,	-155,	-222,	292,	332,	.351,	399.		7.																
Arg	-llD	Glu	Arg	Ser-	Arg-	Gly-	Arg-		7-dr			rg-8.													
Ala-105 to Arg-110,	Ala-114 to Gln-138,	Arg-143 to Glu-155,	Leu-202 to Arg-222,	287 tc	Pro-325 to Arg-332,	Arg-337 to Gly-351,	Pro-389 to Arg-399.		7 to 1			to A													
Ala-1	Ala-1	Arg-	Leu-7	Arg-287 to Ser-292,	Pro-3	Arg-3	Pro-3		Ser-67 to Trp-77.			Pro-3 to Arg-8.													
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Gln-49 to Thr-69,	His-129 to Cys-143.							Glu-1 to Glu-6,	Asn-16 to Arg-22.	Gln-216.to Asp-226,	Thr-250 to Thr-256.														
853							1171	854		855															
770 - 1237							3 - 293	3 - 302		83 - 862								,							
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Asn-89 to Asn-95.	Gln-110 to Asp-120, Ser-189 to Phe-207, Cys-218 to Ser-228, Gln-240 to Ala-245, Glu-263 to Ser-271.
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S0114: 1, H0650:	H0255: 1, S0360:	S0278: 1, H0486: 1	H0318: 1, H0457:	H0039: 1, H0553:	L0763: 1, L0761:	L0764: 1, L0789:	H0144: 1, S0374:	S0310: 1, H0555:	T0445		AR089: 2, AR061:	, H06	H0575: 2, H0090: 2,	L0777: 2, L0757: 2,	S0114: 1, H0650:	H0255: 1, S0360:	S0278: 1, H0486:	H0318: 1, H0046:	H0457: 1, H0039:	H0553: 1, L0763:	L0761: 1, L0764:	L0789: 1, H0144:	S0374: 1, S0310: 1	H0555: 1, L0758: 1	H0445: 1 and S0276:
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Arg-											.ys-21	rp-46	ro-10												
Asp-210 to Arg-216.											Val-14 to Lys-21,	Gln-41 to Trp-46,	Ala-98 to Pro-103.												
Asp-2											Val-1	Gln-4	Ala-9												
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Val-14 to Lys-21, Gln-41 to Trp-46, Ala-98 to Pro-103.	Pro-1 to Thr-8.	Gly-34 to Lys-44, Glu-113 to Glu-118.	lle-94 to Asp-99, Asp-118 to Pro-123, Glu-131 to lle-140, Tyr-143 to Asp-152, Glu-169 to Lys-179. Ala-144 to Glu-151, Thr-162 to Thr-168. Ala-144 to Glu-151, Thr-162 to Thr-168.	
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561	247	248	249	251
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Н0191: 1, Н0027: 1,	H0644: 1, S0028: 1, S0031: 1 and S0260: 1.		AR061: 9, AR089: 3	L0794: 11, S0010: 3,	S0346: 3, L0791: 2,	L0439: 2, L0758: 2,	S0222: 1, T0060: 1,	H0051: 1, S0388: 1,	H0188: 1, S0214: 1,	H0252: 1, L0666: 1,	L0438: 1, L0743: 1,	L0750: 1, L0779: 1,	S0031: 1, L0480: 1,	L0597: 1 and H0667: 1.				L0794: 11, S0010: 3,	S0346: 3, L0791: 2,	L0439: 2, L0758: 2,	S0222: 1, T0060: 1,	H0051: 1, S0388: 1,	H0188: 1, S0214: 1,	H0252: 1, L0666: 1,
	. %	Arg-71 to Asp-76.	Gly-1 to Glu-7,	Gly-30 to Gln-40,	Gly-69 to Gln-75,	Leu-98 to Leu-107,	Tyr-146 to Gly-161,	Arg-179'to Ser-186.							Gly-26 to Gln-36,	Gly-65 to Gln-71,	Leu-94 to Leu-103.	Ala-16 to Thr-21,	Arg-76 to Asn-104,	Ala-123 to Glu-129,	Leu-142 to Glu-147,	Gly-170 to Gln-180,	Gly-209 to Gln-215,	Leu-238 to Leu-247,
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		461 - 895	1 - 735												3 - 728	-		1440 - 283						
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	Tyr-286 to Gly-301,	Arg-319 to Ser-326.			Arg-1 to Arg-6.	Arg-1 to Thr-6,	Pro-8 to Arg-24,	Glu-30 to Lys-35.	,																	
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						Asn-29 to Gly-39,	Pro-49 to Asn-56,	Gln-112 to Ala-119,	Arg-193 to Gln-201,	Leu-222 to Gln-227.	Ser-47 to His-52.				Leu-16 to Ser-32.	Phe-7 to Glu-13,	Gln-46 to Thr-59.						Gln-24 to Arg-44.	Asn-8 to Thr-14,	Gly-38 to Gly-44,
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						480 - 1187					852 - 565	,			48 - 206	193 - 480			83 - 322	560 - 3		-	87 - 284	1150 - 869	
						257					258				292	259			568	260			569	261	
						924848					1150864			7	525926	1121869			525878	1137572			773210	1226988	
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H0069: 1, H0123: 1, L0783: 1, H0521: 1 and L0748: 1.		AR061: 4, AR089: 4	H0318: 1, L0766: 1	and L0748: 1.		AR089: 4, AR061: 2	L0163: 3, H0497: 2,	L0439: 2, H0662: 1,	S0360: 1, L0717: 1,	86016: 1, 80051: 1,	H0428: 1, L0662: 1,	L0768: 1, L0774: 1,	L0776: 1, L0656: 1,	L0789: 1, L0666: 1,	L0743: 1, L0749: 1 and	L0777: 1.		AR061: 4, AR089: 1	L0749: 6, L0794: 5,	H0550: 4, H0575: 4,	H0521: 4, L0601: 4,	H0580: 3, L0761: 3,	L0766: 3, H0402: 2,
	Gln-20 to Arg-26.	Leu-16 to Glu-22,	Tyr-89 to Asn-95.		Pro-15 to Cys-23.	Lys-17 to Phe-26,	Gln-30 to Leu-43.										Asp-3 to Ser-11.	Lys-32 to Val-61,	Pro-83 to Ala-89,	Lys-114 to Gly-120,	Asn-137 to Arg-147,	Gly-186 to Thr-194,	Val-211 to Glu-227,
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Ile-236 to Glu-242,	Phe-254 to Lys-264,	Glu-328 to Leu-334,	Phe-355 to Asn-379,	Thr-434 to Leu-444,	Glu-495 to Leu-502,	Gln-533 to Lys-538,	Ser-586 to Trp-594,	Leu-605 to Glu-611,	Pro-614 to Leu-624,	Thr-626 to Gln-640,	Ser-679 to Ala-684,	Lys-750 to Gly-771,	Glu-840 to Asp-853,	Glu-866 to Glu-874,	Ser-881 to Ala-915,	Asn-929 to Gly-944,	Ala-946 to Thr-953.								
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	Lys-32 to Val-61,	Pro-83 to Ala-89.	Ala-9 to Glu-20, \downarrow	Thr-22 to Gly-32,	Gly-57 to Ser-67,	Arg-125 to Ser-138, H	Gly-167 to Gly-173, IF	Ala-289 to Glu-298, I	Leu-317 to Ala-323, F	Glu-339 to Gly-347, I	Leu-358 to Thr-363, I	Glu-395 to Arg-411,	Ser-446 to Glu-455, F	Glu-475 to Ala-481,	Ser-489 to Leu-497, I-	Ala-501 to Pro-512, F	Asn-520 to Asn-526, S	Ser-546 to Glu-553.		·	: :		<u></u>	<u> </u>	
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H0458: 1, S0140: H0550: 1, H0497: H0575: 1, S0474:	H0421: 1, H0024: H0213: 1, H0087:	H0272: 1, H0641: S0144: 1, L0763: 1	_0761: 1, L0662: 1	.0794: 1, L0803:	.0804: 1, L0659:			, H05	, Ĥ04	and						2, A	3, L(, H06	, H0	, НО	, LO
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L0777: 2, L0759: 2,	H0423: 2, S0218:	H0661: 1, H0305:	H0459: 1, S0360:	H0580: 1, L0717:	H0486: 1, T0074:	H0036: 1, H0051:	S0388: 1, H0039:	H0553: 1, H0124:	H0412: 1, L0770:	T066	L076	L077	C079	S0216: 1, H0682:	H0659: 1, H0670:	S0270: 1, H0540:	L0747: 1, L0780:	L075	L058	H0422: 1		AR08 H04	•	AR08
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H0171: 1, H0383: 1 and S0028: 1.		AR089: 6, AR061: 4	L0749: 2 and H0624:				,	-		AR061: 3, AR089: 3	L0751: 10, L0743: 9,	H0556: 4, S0046: 3,	L0662: 3, L0779: 3,	H0265: 2, S0045: 2,	H0581: 2, H0355: 2,	H0271: 2, H0030: 2,	H0063: 2, S0002: 2,	H0529: 2, L0372: 2,	L0659: 2, L0602: 2,	S0404: 2, L0756: 2,	L0605: 2, H0423: 2,	S0114: 1, H0650: 1,	H0656: 1, L0785: 1,	S0212: 1, H0663: 1,
Gln-19 to Glu-27.		Val-10 to Ser-22,	Ile-26 to Ser-46,	Thr-86 to Asn-91,	His-110 to Asn-119.	Ser-7 to Ile-14,	His-48 to Gln-54,	His-68 to His-74,	Pro-80 to His-87.	Asn-129 to Ser-140,	Glu-164 to Thr-169,	Leu-173 to Ser-184,	Ala-186 to Arg-192,	Lys-239 to Ala-250,	Asp-285 to Gly-291,	Ser-305 to Gln-316,	Thr-334 to Glu-344,	Tyr-350 to Asp-365,	Gln-373 to Lys-382,	Pro-429 to Gly-434,	Gly-510 to Arg-518,	Pro-531 to Arg-539,	Glu-585 to Leu-593,	Gln-669 to Ser-674,
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H0662: 1, H0306: 1,	80358: 1, 80132: 1,	H0437: 1, H0549: 1,	H0609: 1, H0610: 1,	H0602: 1, H0587: 1,	H0333: 1, H0559: 1,	H0486: 1, H0013: 1,	H0069: 1, H0635: 1,	H0156: 1, H0575: 1,	H0590: 1, H0318: 1,	H0052: 1, H0046: 1,	H0457: 1, H0081: 1,	H0083: 1, H0247: 1,	H0284: 1, H0615: 1,	L0194: 1, H0031: 1,	H0038: 1, H0551: 1,	H0272: 1, H0494: 1,	H0625: 1, H0641: 1,	L0763: 1, L0769: 1,	L0761: 1, L0772: 1,	L0771: 1, L0773: 1,	L0648: 1, L0767: 1,	L0768: 1, L0794: 1,	L0766: 1, L0774: 1,	L0375: 1, L0607: 1,	L0788: 1, L0665: 1,
Pro-693 to Ile-700,	Pro-795 to Gly-801.					*					*			<											
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		*			-			Asn-128 to Ser-139,	Glu-163 to Thr-168,	Leu-172 to Ser-182.	Lys-7 to Thr-16,	Lys-33 to Asn-41,	Glu-52 to Arg-63.		•										
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										,			Gly-43 to Tyr-50.								•		Asn-36 to Gly-43,	Gly-66 to Glu-73,	Ser-86 to Pro-92,
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L0755: 2, L0759: 2,	S0342: 1, S6024: 1,	S0376: 1, L0021: 1,	H0150: 1, T0003: 1,	H0014: 1, L0764: 1,	L0794: 1, L0803: 1,	L0783: 1, L0809: 1,	L0666: 1, L0665: 1,	L0438: 1, L0749: 1,	L0779: 1, L0777: 1,	L0758: 1, L0604: 1,	S0026: 1 and H0423: 1.		AR089: 7, AR061: 3	L0731: 3, H0395: 2,	L0764: 2, L0794: 2,	H0521: 2, T0049: 1,	H0650: 1, S0140: 1,	L0021: 1, H0083: 1,	H0271: 1, L0769: 1,	L0761: 1, L0646: 1,	L0771: 1, L0803: 1,	L0804: 1, L0775: 1,	L0519: 1, H0445: 1,	L0588: 1 and H0542: 1.	
Asn-124 to Leu-133.								,				Asn-18 to Arg-23.	Ser-47 to Thr-54,	Asn-62 to Asp-67,	Pro-109 to Ser-114,	Arg-146 to Arg-153.				r			·		Pro-27 to Lys-34,
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Glu-49 to Asn-59,	Lys-70 to Lys-82,	Gly-99 to Cys-116.	Glu-4 to Leu-11,	Gln-30 to Cys-40,	Pro-53 to Pro-59,	Thr-99 to Ser-104.	Met-22 to Trp-27.	Gln-13 to Ile-29.		,	Gln-13 to Ile-29.	Gln-1 to Thr-6.									- O				
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Asp-73 to Ser-80,	Arg-104 to Asp-115,	Glu-195 to Pro-202.									· ·						٠.								
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	Asn-1 to Asp-8,	Cys-12 to Gln-17,	Lys-47 to Thr-57,	Leu-77 to Gly-92,	Gln-153 to Arg-160.	Glu-1 to Arg-6,	Ser-11 to Val-17,	Gln-42 to Arg-54.		Ser-32 to Glu-39,	Ala-60 to Trp-69.										,
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L0593; 1, S0011: 1, H0668: 1, H0542: 1, H0423: 1, H0422: 1, S0456: 1 and H0352: 1.			AR061: 2, AR089: 2	· H0441: 3, L0794: 2,	L0805: 2, L0764: 1 and	L0521: 1.	*	AR089: 3, AR061: 1	L0439; 4, L0769; 2,	L0662: 2, L0592: 2,	S0046: 1, H0618: 1,	H0545: 1, S0388: 1,	S0051: 1, H0355: 1,	H0264: 1, H0561: 1,	L0770: 1, L0372: 1,	L0508: 1, H0547: 1,	H0689: 1, L0731: 1 and	L0758: 1.	1	AR061: 7, AR089: 6	L0766: 4, H0620: 3,	L0663: 3, L0749: 3,
	Lys-11 to Ala-39,	Ser-52 to Asp-57.	Lys-50 to Lys-56,	Thr-77 to Arg-87.			Ser-9 to Lys-14.	Arg-151 to Thr-159,	Arg-168 to Lys-173,	Glu-181 to His-190,	Phe-237 to Asn-242,	Asp-267 to Glu-274,	Tyr-283 to Pro-300,	Pro-306 to Trp-311,	Ala-371 to Asp-383.		-	:		Pro-16 to Leu-22,	Arg-32 to Gln-37,	Thr-55 to Thr-72,
	1203		895				1204	968				-							1205	897		
,	3 - 257		351 - 674				3 - 200	216 - 1364		,							-		205 - 510	1 - 234		
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L0731: 3, S0026: 3,	S0422: 2, L0764: 2,	L0655: 2, L0606: 2,	L0665: 2, L0439: 2,	L0759: 2, S0114: 1,	H0650: 1, H0369: 1,	H0600: 1, H0581: 1,	H0421: 1, H0271: 1,	H0615: 1, H0591: 1,	H0038: 1, H0040: 1,	H0063: 1, H0494: 1,	L0598: 1, L0520: 1,	L0761: 1, L0662: 1,	L0767: 1, L0649: 1,	L0803: 1, L0775: 1,	L0805: 1, L0809: 1,	L0664: 1, L0438: 1,	H0658: 1, H0672: 1,	H0436: 1, L0747: 1 and	50196: 1.	AR061: 4, AR089: 3	L0766: 5, L0806: 3,	T0010: 2, L0761: 2,	L0752: 2, H0677: 2,	S0278: 1, H0486: 1,	S0038: 1, L0796: 1,
				•																Ser-1 to Ser-10,	Ser-23 to Asp-38,	Arg-67 to Lys-73,	Ser-181 to Asp-187,	Asp-222 to Ser-233,	Pro-248 to Asn-253.
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ſ	L0644: 1, L0771: 1,	L0659: 1, L0666: 1,	L0664: 1, H0521: 1,	L0779: 1, H0445: 1 and.	L0595: 1.			AR061: 77, AR089: 30	S0136: 3, S0036: 1 and	S0144: 1.						AR061: 10, AR089: 5	S0328: 4, S0218: 3,	H0040: 2, L0438: 2,	L0439: 2, H0624: 1,	H0431: 1, L0021: 1,	S0049: 1, H0266: 1,	H0090: 1, H0561: 1,	S0422: 1, H0529: 1,	L0659: 1, S0126: 1,	S0027: 1, S0028: 1,	S0206: 1, L0748: 1,
						Ser-1 to Ser-10,	Ser-23 to Asp-38.	Pro-45 to Ser-50,	Thr-54 to Ile-64,	Lys-205 to Arg-211,	Pro-214 to Gly-220,	Asp-296 to Asp-301,	Pro-355 to Glu-367,	Thr-391 to Glu-396.	Leu-33 to Phe-38.	Pro-39 to Glu-45,	Pro-102 to Arg-107,	Tyr-121 to Lys-128,	Gln-140 to Ile-169,	Arg-269 to Gly-285,	Lys-313 to Gly-320,	Ala-344 to Thr-350,	Arg-356 to Gln-365,	Tyr-373 to His-380,	Arg-392 to Leu-399,	Leu-403 to Gln-408.
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	Phe-3 to Phe-8, Pro-30 to Glu-36, Pro-93 to Arg-98.	Ser-41 to Glu-47, Arg-71 to Leu-85, Asp-87 to Glu-97.	Glu-15 to His-24, Asn-47 to His-53.	Gin-1 to Gly-7, Ser-63 to Gly-68, Pro-74 to Cys-81. Glu-1 to Glu-22.	Asp-29 to Arg-35, Leu-58 to Thr-64. Asp-29 to Arg-35, Leu-58 to Thr-64.	lle-34 to Gly-42.
	1208	106	1209	902	903	904
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	792383	1150833	681745	1076509	1162086	1105244
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AR089: 1, AR061: 1 S0136: 2		AR089: 7, AR061: 6	L0769: 16, L0776: 16,	L0742: 13, L0745: 13,	L0754: 12, L0748: 11,	L0439: 11, L0747: 10,	L0805: 8, L0438: 6,	L0731: 6, L0764: 5,	L0806: 5, L0749: 5,	L0779: 5, L0752: 5,	L0771: 4, H0052: 3,	L0796: 3, L0761: 3,	L0741: 3, L0756: 3,	L0753: 3, L0758: 3,	S0360: 2, H0013: 2,	H0068: 2, T0041: 2,	L0768: 2, L0659: 2,	L0783: 2, L0809: 2,	H0670: 2, L0746: 2,	L0591: 2, H0265: 1,	H0686: 1, H0583: 1,	H0657: 1, L0785: 1,	H0662: 1, S0418: 1,
Asp-36 to Lys-42.	Leu-7 to Gln-17.	Thr-56 to Gly-62,	Glu-72 to Gly-81.		-			,															
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Thr-56 to Gly-62,	Glu-72 to Gly-81. Thr-48 to Arg-54,	Pro-149 to Ser-155. Ser-14 to Lys-19.	,		*	*		Pro-26 to Gly-32,	Ala-133 to Cys-138,	Asp-145 to Lys-152,	Leu-164 to Ser-173,	Lys-178 to Ser-183,	Asp-260 to Phe-266.	Pro-26 to Gly-32.	Ser-27 to Glu-35,	Thr-43 to Phe-52,	Val-59 to Gln-70,	His-74 to Val-79,
1214	206	1215	806				1216	606						1217	910			
285 - 680	547 - 29	127 - 273	713 - 438				117 - 284	2 - 931			-			2 - 286	478 - 2028	-		-
109	294	602	295				603	296						604	297			
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					AR089: 0, AR061: 0	S0218: 1, H0264: 1 and	S0053: 1.		AR061: 1, AR089: 0	H0556: 10, L0748: 8,	H0620: 7, L0747: 7,	L0637: 5, H0265: 4,	H0013: 4, H0551: 4,	L0776: 4, L0663: 4,	L0596: 4, H0622: 3,	H0617: 3, L0772: 3,	L0766: 3, S0126: 3,	L0751: 3, L0752: 3,	S0031: 3, L0593: 3,	H0657: 2, S0360: 2,	S0222: 2, T0115: 2,	H0009: 2, L0471: 2,	H0594: 2, H0288: 2,	H0039: 2, H0424: 2,	H0135: 2, H0040: 2,
Pro-108 to Lys-122,	Ala-130 to Phe-141,	Val-145 to Ala-151,	Asp-159 to Glu-165,	Ser-185 to Lys-191.	Glu-55 to His-72.				lle-45 to Arg-52,	Phe-77 to Pro-85,	Leu-111 to Val-118,	Ile-124 to Thr-129,	Pro-139 to Gly-151,	Arg-186 to Gly-215,	Lys-223 to Glu-230.										
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H0623: 2, L0763: 2,	_0769: 2, L0796: 2,	04: 2, L0775: 2,	34: 2, L0666: 2,	L0438: 2, L0756: 2,	.0757: 2, H0445: 2,	.0595: 2, H0542: 2,	H0423: 2, H0422: 2,	F0002: 1, S0114: 1,	S0218: 1, H0661: 1,	S0358: 1, S0007: 1,	S0046: 1, S0132: 1,	S0278: 1, H0431: 1,	H0370: 1, H0586: 1,	H0632: 1, H0486: 1,	F0040: 1, S0280: 1,	H0318: 1, H0581: 1,	H0085: 1, T0110: 1,	H0545: 1, H0081: 1,	S0362: 1, H0247: 1,	H0266: 1, H0290: 1,	H0292: 1, H0286: 1,	S0340: 1, S0036: 1,	H0090: 1, H0591: 1,	H0038: 1, H0616: 1,	H0433-1 H0412-1
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S0038: 1, H0561: S0352: 1, S0144: 1	S0142: 1, L0369:	.0761: 1, L0372:	: 1, LO	L0764: 1, L0771: 1	: 1, LO	: 1, LO	.0651: 1, L0378:	.0657: 1, L0658:	.0383: 1, L0665:	.0352: 1, H0593:	H0689: 1, H0682:	H0660: 1, S0328:	H0696: 1, S0044:	: 1, S30	: 1, L0 ²	1, LO	L0750: 1, L0731:		L0362: 1, L0361:	H0653: 1, H0136:	1, H0	<u>-</u>		
\$0038 \$0352	S0142	L0761	L0646	L0764	L0773	L0388	L0651	L0657	L0383	L0352	6890H	D990H	9690H	S0037: 1, S3014: 1,	S0206	L0754	L0750	L0759	L0362	H0653	9610S	S0424:		
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				AR061: 2, AR089: 2	H0253: 1, S0010: 1,	L0456: 1, H0695: 1 and	L0657: 1.	-			AR089: 8, AR061: 5	H0264: 2 and L0367:		AR061: 7, AR089: 2	H0253: 10, H0617: 8,	H0559: 7, H0265: 6,	H0618: 5, H0551: 5,	H0052: 4, H0620: 4,	L0794: 4, H0556: 3,	H0135: 3, H0087: 3,	L0659: 3, L0666: 3,	L0663: 3, L0438: 3,	H0522: 3, L0749: 3,
Cys-59 to Thr-68,	Pro-93 to Gly-105,	Arg-140 to Gly-169,	Lys-177 to Glu-184.	Gln-5 to His-17,	Pro-30 to Ser-40,	Pro-42 to Thr-65,	Gly-102 to Gln-107,	Ala-112 to Lys-118,	Ser-127 to Thr-138.					Gly-50 to Asp-59,	Thr-220 to Phe-233,	Glu-285 to Tyr-291,	Thr-298 to Arg-303,	Ala-353 to Asn-358.			-	٠	,
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171: 2	341: 2	255: 2	60: 2	50: 2	51:2	124: 2	40:2	44: 2	62: 2	83: 2	96: 2	51: 2	31:2	05: 2	01:2	59: 1	56: 1	37: 1	51: 1	41: 1	92: 1	97: 1	57: 1	35: 1	42: 1
磿	H03	H02	803	H05	H0C	H04	H00	S03	907	L07	90H	L07	L07	F06	F06	H01	90H	90H	H03	H0H	H05	H04	H02	H06	00H
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											Arg-1 to Thr-15.				-						·				-
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											3 - 500	1367 - 1624					,-	,		1286 - 1564	3 - 203				
					٠						609	303						٠		610	304				
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AR089: 23, AR061: 6 L0518: 4, L0731: 3, L0637: 2, H0659: 2, H0170: 1, S6024: 1, S0360: 1, H0586: 1, H0050: 1, L0598: 1, L0763: 1, L0666: 1, L0663: 1, L0743: 1,	LU/45: 1 and LU601: 1.	AR089: 1, AR061: 1	H0553: 3, S0360: 1,	H0561: 1, L0526: 1,	H0519: 1, S0126: 1,	H0543: 1 and L0697: 1.						*	AR061: 4, AR089: 4	L0361: 2, H0662: 1,	T0039: 1, H0156: 1,	H0052: 1, H0194: 1,]н0179: 1, Н0135: 1,
		Gly-1 to Pro-6,	His-18 to Ser-23,	Asn-45 to Thr-56,	Ala-65 to Arg-70,	Asp-84 to Ile-89,	Glu-109 to Leu-114,	Lys-146 to Lys-155.	His-12 to Ser-17,	Asn-39 to Thr-50,	Ala-59 to Arg-64,	Asp-78 to Ile-83.	Ser-25 to Asp-40,	Pro-47 to Glu-54,	Pro-146 to Gly-153,	Pro-194 to Thr-200.	
918	1224	616							1225	,	-		920				
338 - 508	338 - 475	2 - 466						*	1 - 996				428 - 1027				
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		Ser-33 to Ala-47.	Ala-16 to Ser-22,	Pro-31 to Leu-38,	Ser-41 to Gly-48.								Arg-3 to Asp-14,	Glu-53 to Gly-59,	Asp-105 to Asn-113.	Thr-6 to Asp-14,	Ser-36 to Glu-41,	Ala-159 to Trp-168,	Ser-176 to Lys-181.		
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										,					Pro-10 to Lys-22.			Lys-31 to Ser-37,	Leu-112 to Ser-119.				Gly-59 to Glu-66,	Cys-87 to Asn-93,	Asn-122 to Trp-127,
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Arg-129 to Ser-134,	Ala-144 to Asp-149,	Asn-176 to Ala-182.	Ala-1 to Gly-10.			Leu-52 to Leu-66,	Trp-97 to Leu-103.												Thr-5 to Asn-13,	Pro-69 to Ala-76.				-	Arg-9 to Pro-16.
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H0634: 1 and H0522:	<u> </u>		,						AR061: 6, AR089: 2	H0194: 2, L0748: 2,	H0052: 1, T0010: 1,	H0658: 1, S0380: 1 and	L0366: 1.											20	
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	Asp-52 to Thr-62, Thr-101 to Trp-112, Gly-131 to Asn-141, Asp-173 to Ile-179.	Val-14 to Val-19, Ser-27 to Ser-32.	Gln-13 to Lys-19, Gln-59 to Tyr-69, Asp-116 to His-126, Gly-164 to Lys-170, Gln-182 to Gly-187, Tyr-207 to Gly-212.
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	Gly-1 to Leu-26,	Thr-28 to Leu-35.		_								*												*	-
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H0318.2, H0052.2, H0309.2, H0263.2, H0046.2, S0050.2, S0022.2, S0214.2, H0428.2, H0622.2, H0031.2, H0533.2, H0031.2, H0533.2, H0031.2, H0650.2, S0036.2, H0064.2, H00413.2, H0660.2, L0369.2, L0360.2, L0374.2, L0360.2, L0369.2, L0360.2, L0377.2, L0360.2, H0519.2, H0648.2, H0648.2, H0678.2, S0027.2, L0369.2, L0368.2, L0369.2, L0368.2, L0369.2, L0368.1, H0685.1, H0686.1, H0685.1, H0686.1, R0369.2, L0369.2, R0369.2, R0			-		<u> </u>										-											
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S6024: 1 and S0196: 1.	AR061: 1, AR089: 0	AR089: 7, AR061: 6	H0046: 2, L0744: 2,	H0581: 1 and H0547: 1.															-					
	Gln-1 to Gly-11.																							
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AR089: 6, AR061: 4 L0749: 6, L0794: 4, H0123: 1, L0768: 1 and S0194: 1	AR089: 7, AR061: 3 L0754: 6, L0439: 2, L0751: 2, L0747: 2, H0661: 1, H0402: 1, H0272: 1, L0438: 1, H0696: 1 and L0779: 1.	AR089: 0, AR061: 0 L0792: 2, S0420: 1, H0645: 1, H0494: 1, L0806: 1, L0807: 1, L0740: 1 and L0752: 1.	_ p	AR054: 2, AR051: 1, AR061: 0, AR089: 0, AR050: 0 S0001: 1, H0191: 1 and S0044: 1.
	Thr-1 to Leu-11, Lys-24 to Ile-29, Gln-134 to Asn-144, Gln-150 to Thr-165.	Lys-20 to Ser-28, Arg-44 to Ala-52, Leu-83 to Glu-89.		Lys-213 to Gly-220.
945	946	947	948	949
3 - 443	1 - 498	2 - 463	3 - 476	148 - 807
332	333	334	335	336
670041	699379	705332	734474	772553
HFTAR20	HCUFD32	НКАЕО39	HLWBR95	HPWCJ63
322	323	324	325	326

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	AR089: 8, AR061: 4	L0743: 2, S0040: 1,	H0663: 1, H0427: 1,	H0545: 1, S0250: 1,	H0087: 1, S0038: 1,	L0804: 1 and L0783: 1.	AR089: 1, AR061: 1	H0619: 2, L0779: 2,	S0222: 1, H0530: 1,	H0433: 1, L0766: 1 and	L0753: 1.	AR061: 4, AR089: 2	S0010: 3, S0036: 3,	L0766: 3, S0222: 2,	S0346: 2, H0310: 2,	H0327: 2, H0457: 2,	H0656: 1, S0282: 1,	S6016: 1, S0665: 1,	L2250: 1, H0051: 1,	S0386: 1, H0342: 1,	S0031: 1, L0366: 1 and	H0543: 1.	AR089: 6, AR061: 3	S0282: 1, T0040: 1,	H0013: 1, S0182: 1,
Lys-213 to Gly-220.												Lys-26 to Gln-36,	Leu-50 to Glu-56,	Gly-93 to Thr-106,	Gln-108 to Gly-122,	Gly-132 to Gln-138,	Ser-144 to Trp-153,	Glu-155 to Glu-171,	Lys-178 to Pro-198,	Val-207 to Asn-230,	Arg-235 to Asp-247.		Lys-22 to Gly-27.		
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S0426: 1, H0670: 1,	H0667: 1 and H0542: 1.	AR089: 21, AR061: 10	H0156: 1, H0575: 1,	H0590: 1, H0263: 1 and	L0362: 1.	AR089: 1, AR061: 1	S0212: 1 and H0040: 1.	AR054: 16, AR051:	13, AR061: 8, AR089:	3, AR050: 1	H0040: 1, H0022: 1,	S0152: 1 and H0521: 1.			AR089: 10, AR061: 6	H0619: 1, S0036: 1,	H0135: 1 and H0520: 1.			AR089: 1, AR061: 0	S0358: 1, H0642: 1 and	H0264: 1.	AR089: 9, AR061: 5	80192: 2, 80222: 1,	H0562: 1, H0373: 1 and
							7	Arg-37 to Arg-44,	Asn-47 to Glu-56,	Lys-65 to Glu-70,	Arg-78 to Pro-83,	Gln-98 to Asp-106,	Pro-142 to Ile-151,	Ala-154 to Thr-180.	Glu-11 to Ser-21,	Asn-52 to Ser-57,	Arg-81 to Met-88,	Glu-139 to Tyr-146,	Glu-153 to Leu-159.				Asp-51 to His-60,	Thr-105 to Pro-117,	Asp-143 to Ala-151,
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		6 - 701				2 - 538		3 - 644							81 - 584					283 - 2			64 - 2151		
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		911292				911449		911454	,			*			911456					911459			919878		
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Asp-167 to Ile-192,	Ala-212 to Thr-223,	Arg-325 to Asp-346,	Lys-354 to Glu-359,	Gln-390 to Asp-395,	Arg-406 to Ser-412,	Gln-431 to Asp-438,	Ser-447 to Leu-465,	Arg-516 to Thr-522,	Lys-561 to Ser-570,	Pro-583 to Pro-589,	Tyr-625 to Asn-631,	Pro-644 to Arg-650.	Glu-19 to Asp-28,	Tyr-37 to Ala-42,	Pro-53 to Leu-59,	lle-67 to Gly-74,	Arg-152 to Val-158.								
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									Ser-3 to Asp-8,	Ser-39 to Pro-61,	Ser-63 to Ser-69,	Lys-144 to Thr-150,	Asp-187 to Gly-193.					,								
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				<u>.</u>					Pro-8 to Arg-29,	Tyr-156 to Asp-161,	Glu-172 to Pro-184,	Arg-194 to Asn-203.												,	
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S0152: 1, S0260: 1 and	L0366: 1.	AR061: 10, AR089: 4	L0789: 6, L0809: 2,	H0669: 1, H0369: 1,	H0252: 1, L0055: 1,	L0763: 1, L0770: 1,	L0638: 1, L0803: 1,	L0805: 1, L0776: 1,	L0753: 1, L0758: 1,	L0592: 1 and H0543: 1.	AR089: 16, AR061: 5	L0439: 10, L0526: 6,	L0005: 5, L0740: 5,	S0422: 4, L0438: 4,	L0758: 4, L0581: 4,	H0370: 3, H0486: 3,	S0003: 3, H0144: 3,	H0659: 3, H0672: 3,	L0744: 3, L0754: 3,	L0731: 3, L0595: 3,	H0657: 2, H0664: 2,	80418: 2, 80376: 2,	H0431: 2, H0050: 2,	L0471: 2, H0083: 2,	H0266: 2, H0090: 2,
		Pro-1 to Pro-12,	Pro-53 to Gly-58,	Gly-65 to Ser-71,	Gly-106 to Lys-111,	Lys-143 to Gly-163.					Pro-53 to Val-58,	Pro-85 to Ser-95,	Gln-132 to Gly-138.							-					
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						,		•								C.				Arg-11 to Arg-18,	Glu-23 to Glu-28,	Asn-40 to Leu-45,	Thr-53 to Asp-58,	Lys-74 to Asp-82,	Val-92 to Glu-97,
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S0274: 2, L0754: 2,	L0604: 2, S0202: 1,	S0252: 1, S0360: 1,	H0550: 1, H0600: 1,	H0333: 1, H0486: 1,	H0013: 1, H0427: 1,	H0599: 1, H0575: 1,	S0010: 1, H0194: 1,	H0327: 1, H0569: 1,	H0594: 1, S6028: 1,	S0250: 1, H0622: 1,	L0544: 1, H0144: 1,	L0438: 1, H0519: 1,	S0126: 1, L0744: 1,	L0747: 1, L0777: 1,	S0242: 1 and S0196: 1.	AR050: 18, AR089: 2,	AR061: 2, AR051: 2,	AR054: 1	S0114: 1, H0069: 1,	H0014: 1, L0667: 1,	L0804: 1, L0659: 1,	S0052: 1 and H0422: 1.	AR089: 70, AR061:	14, AR050: 9, AR051:	1, AR054: 1
Ser-104 to Asn-109,	Asp-127 to Phe-133,	Gln-158 to Asp-170,	Asn-177 to Ala-207.													Ile-5 to Lys-10,	Arg-78 to Asp-92.				-		Lys-82 to Gln-87,	Asp-103 to Ala-108,	Glu-122 to Lys-127.
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L0766: 2, H0575: 1,	H0264: 1, L0761: 1 and	L0804: 1.	AR089: 1, AR061: 0	H0305: 4, L0731: 3,	L0581: 3, H0622: 2,	H0059: 2, L0764: 2,	L0766: 2, L0741: 2,	L0740: 2, L0749: 2,	H0423: 2, H0149: 1,	H0159: 1, S0114: 1,	H0656: 1, H0255: 1,	H0306: 1, H0402: 1,	S0045: 1, H0351: 1,	H0550: 1, H0441: 1,	H0036: 1, T0048: 1,	H0318: 1, H0581: 1,	H0024: 1, H0051: 1,	H0083: 1, H0510: 1,	H0617: 1, H0412: 1,	H0280: 1, H0647: 1,	L0646: 1, L0374: 1,	L0385: 1, L0662: 1,	L0767: 1, L0794: 1,	L0649: 1, L0774: 1,	L0806: 1, L0653: 1,
			His-14 to Gln-19.							. •															
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L0657: 1, L0659: 1,	L0783: 1, S0126: 1,	H0690: 1, H0670: 1,	H0672: 1, S0328: 1,	S0380: 1, H0555: 1,	L0748: 1, L0752: 1,	L0758: 1, S0194: 1,	H0542: 1 and H0422: 1.	AR089: 1, AR061: 0	L0591: 20, L0748: 13,	H0090: 5, H0521: 4,	L0758: 4, H0556: 3,	H0656: 3, S0358: 3,	H0038: 3, S0002: 3,	L0794: 3, L0766: 3,	L0803: 3, L0805: 3,	L0791: 3, L0665: 3,	H0547: 3, S0328: 3,	L0747: 3, H0423: 3,	H0624: 2, S0420: 2,	S0046: 2, H0427: 2,	H0156: 2, H0046: 2,	L0471: 2, H0510: 2,	H0424: 2, H0181: 2,	H0264: 2, H0100: 2,	S0426: 2, L0631: 2,
								Phe-20 to Lys-37,	Asn-108 to Arg-116.	,								,							
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H0539: 2, S0380: 2,	S0152: 2, H0555: 2,	S3014: 2, S0206: 2,	L0777: 2, L0731: 2,	H0422: 2, H0686: 1,	L0002: 1, H0657: 1,	H0663: 1, H0662: 1,	S0348: 1, S0360: 1,	S0007: 1, S0278: 1,	H0600: 1, H0497: 1,	H0559: 1, T0039: 1,	H0013: 1, H0599: 1,	H0575: 1, H0004: 1,	H0318: 1, H0581: 1,	H0421: 1, H0263: 1,	H0050: 1, H0082: 1,	H0373: 1, H0071: 1,	H0629: 1, S0003: 1,	H0328: 1, H0031: 1,	H0553: 1, H0111: 1,	H0628: 1, H0617: 1,	H0673: 1, S0364: 1,	H0135: 1, H0163: 1,	T0067: 1, H0561: 1,	S0440: 1, S0344: 1,	L0761: 1, L0764: 1,
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L0771: 1, L0773: 1,	L0650: 1, L0776: 1,	L0655: 1, L0606: 1,	L0629: 1, L0659: 1,	L0809: 1, L0792: 1,	L0666: 1, H0520: 1,	H0593: 1, H0689: 1,	H0659: 1, S0330: 1,	H0522: 1, H0627: 1,	L0742: 1, L0439: 1,	L0740: 1, L0749: 1,	L0779: 1, L0752: 1,	L0757: 1, L0759: 1,	H0445: 1, L0485: 1,	H0653: 1, S0196: 1,	H0542: 1 and H0506: 1.	AR054: 115, AR050:	108, AR051: 87,	AR061: 4, AR089: 2	H0644: 3, S0408: 1,	S0280: 1, H0620: 1,	S0364: 1, L0637: 1,	L0764: 1, S0044: 1,	L0611: 1, L0777: 1,	L0755: 1, L0731: 1 and	S0194: 1.
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AR089: 2, AR061: 2	L0659: 8, L0666: 8,	L0751: 7, L0665: 6,	.0528: 5, L0743: 5,	.0663: 4, H0052: 3,	L0638: 3, L0646: 3,	L0764: 3, L0662: 3,	L0774: 3, L0747: 3,	H0668: 3, S0192: 3,	H0150: 2, H0620: 2,	H0413: 2, H0649: 2,	S0426: 2, L0763: 2,	L0769: 2, L0648: 2,	L0766: 2, L0653: 2,	L0657: 2, S0126: 2,	H0670: 2, L0754: 2,	L0749: 2, H0685: 1,	S0040: 1, H0650: 1,	S0212: 1, H0255: 1,	S0420: 1, S0045: 1,	H0261: 1, H0391: 1,	L0022: 1, H0581: 1,	H0597: 1, H0544: 1,	H0545: 1, H0123: 1,	H0012: 1, H0024: 1,	H0188: 1, S0250: 1,
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L0483: 1, H0617: 1, H0551: 1, H0494: 1, S0210: 1, L0372: 1, L0643: 1, L0773: 1, L0643: 1, L0573: 1, L0775: 1, L0375: 1, L0776: 1, L0661: 1, L0629: 1, L0664: 1, S0053: 1, L0664: 1, S0053: 1, H0648: 1, H0672: 1, H0539: 1, H0672: 1, H0539: 1, L0753: 1, L0752: 1, L0753: 1, L0752: 1, L0758: 1, L0592: 1, L0758: 1, L0693: 1 and H0352: 1,		AR089: 30, AR061: 6 H0081: 1, H0087: 1, S0144: 1 and H0538: 1.	39: 6, AR061: 2
L0483: H0551: S0210: L0643: L0643: L0775: L0651: L0776: L0629: S0053: H0658: H0658: H0672:		AR08 H00 S014	AR089;
	Gln-56 to Pro-70, Gly-78 to Gly-87.	Leu-7 to Ala-13.	
	1232	7.26	978
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		354	355

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H0663: 2, S0328: 2,	S0420: 1, S0046: 1,	H0559: 1, T0082: 1,	H0050: 1, H0100: 1,	H0494: 1, L0640: 1,	L0789: 1, H0436: 1 and	L0439: 1.	AR089: 8, AR061: 2	HØ556: 1, S0040: 1,	H0657: 1, H0306: 1,	H0393: 1, H0050: 1,	H0266: 1, H0112: 1,	Ĥ0063: 1, S0142: 1,	S0002; 1, L0794: 1,	L0378: 1, L0655: 1,	L0791: 1, L0665: 1,	H0539: 1, H0521: 1,	L0596: 1, L0593: 1,	L0595: 1 and H0653: 1.	AR089: 2, AR061: 1	L0766: 26, L0439: 11,	L0757: 8, H0521: 5,	L0748: 5, H0462: 4,	L0745: 4, L0777: 4,	H0013: 3, H0123: 3,	L0774: 3, H0522: 3,
*												,							Pro-1 to Gly-7,	Arg-15 to Trp-21,	Pro-58 to Asn-63,	Arg-82 to Gly-88.			
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L0752: 3, S0356: 2,	S0222:	H0431: 2, H0427: 2,	H0052: 2, H0545: 2,	.0770: 2, L0769: 2,	.0768: 2, L0806: 2,	10144:	L0751: 2, L0756: 2,	.0591:	.0593: 2, H0667: 2,	H0677: 2, H0656: 1,	\$0358:	30045:	10486:	H0546: 1, S0022: 1,	S0214: 1, H0328:	H0615: 1, H0428:	F0023: 1, H0628:	L0055: 1, H0032:	H0090: 1, H0059:	H0100: 1, L0351:	S0144: 1, S0002:	L0598: 1, L0764:	L0771: 1, L0662:	L0794: 1, L0775: 1	L0805: 1, L0545: 1
52: 3, 9	61: 2,	31: 2,]	52: 2,]	70: 2, 1	68: 2, I	59: 2, I	51: 2, I	79: 2, I	93: 2, I	77: 2, 1	61: 1,	80: 1, 9	70: 1, 1	46: 1, 9	14: 1, F	15: 1, 1	23: 1, F	55: 1, F	90: 1, I	00: 1, 1	4: 1, S	98: 1, L	71: 1, I)4: 1, L)5: 1, L
L07	H02	H04	H00	L07	L07	F06.	L07	L07	L059	90H	90H	H05	H03	H05	S02	90H	T00	,00 <u>7</u>	H00	H01	S01 ²	L059	L077	L07)80T
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L0543: 1, L0789: 1,	L0790: 1, L0791: 1,	L0792: 1, L0663: 1,	H0520: 1, H0547: 1,	H0519: 1, H0648: 1,	L0740: 1, L0746: 1,	L0747: 1, L0750: 1,	L0759: 1, L0608: 1,	L0601: 1, S0026: 1,	H0665: 1, H0136: 1 and	S0242: 1.	AR089: 24, AR061: 6	S0134: 1, L0749: 1,	L0759: 1, S0260: 1 and	L0596: 1.		AR089: 15, AR061: 5	S0360: 2, L0766: 2,	L0747: 2, T0002: 1,	H0686: 1, H0662: 1,	S0046: 1, H0023: 1,	H0560: 1, H0647: 1,	L0662: 1, L0666: 1,	H0576: 1, L0779: 1,	L0596: 1, L0590: 1,	L0601: 1 and H0667: 1.
						ì					Thr-1 to Asp-19,	Cys-23 to Cys-34,	Gln-36 to Gln-58,	Leu-78 to Gly-87,	Asp-164 to His-169.	Arg-1 to Gly-10.	-								,
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AR089: 15, AR061: 7	AR061: 1, AR089: 1	L0438: 12, L0439: 11,	H0617: 5, H0556: 4,	H0618: 3, H0253: 3,	.0769: 3, L0761: 3,	.0759: 3, H0544: 2,	H0031: 2, H0135: 2,	H0038: 2, H0641: 2,	0764: 2, L0783: 2,	.0809: 2, L0790: 2,	L0666: 2, L0663: 2,	.0665: 2, H0144: 2,	S0330: 2, L0751: 2,	L0779: 2, H0543: 2,	H0265: 1, H0685: 1,	H0657; 1, H0306; 1,	S0420: 1, S0354: 1,	S0360: 1, S0046: 1,	L0717: 1, H0550: 1,	H0592: 1, H0333: 1,	H0331: 1, H0559: 1,	H0486: 1, H0013: 1,	H0244: 1, H0635: 1,	Н0575: 1, Н0596: 1,
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T0110: 1, H0123: 1,	H0615: 1, H0033: 1,	H0553: 1, H0212: 1,	H0124: 1, H0040: 1,	H0616: 1, H0264: 1,	H0488: 1, H0100: 1,	H0494: 1, H0131: 1,	H0529: 1, L0637: 1,	L0772: 1, L0766: 1,	L0775: 1, L0375: 1,	L0776: 1, L0628: 1,	L0657: 1, L0664: 1,	S0374: 1, H0547: 1,	H0593: 1, S3014: 1,	S0027: 1, L0748: 1,	L0750: 1, L0731: 1,	L0758: 1, H0595: 1,	S0276: 1 and H0423: 1.	AR089: 4, AR061: 2	H0521: 17, S0007: 11,	L0747: 11, H0543: 8,	S0278: 7, H0581: 7,	S0344: 7, L0766: 7,	L0745: 7, H0556: 6,	L0769: 6, L0748: 6,	L0731: 6, L0601: 6,
										٠,		•	٠					Gln-24 to Gly-30,	Asp-57 to Lys-62,	Leu-109 to Thr-115,	Asn-153 to Gln-166,	Gly-168 to Glu-173,	Gln-184 to Ala-199,	Gly-221 to Pro-232,	Pro-234 to Pro-243,
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L0157: 5,	H0424: 5, L0758: 5,	S0049: 4,	H0050: 4,	H0135: 4, L0666: 4,	H0522: 4, H0436: 4,	L0439: 4, L0750: 4,	H0423: 4, T0002: 3,	H0656: 3, S0001: 3,	H0619: 3, H0617: 3,	T0042: 3, S0142: 3,	L0770: 3,	L0761: 3, L0378: 3,	.0659: 3, L0665: 3,	H0422: 3, H0171: 2,	H0650: 2, L0005: 2,	H0645: 2, H0455: 2,	H0156: 2, H0575: 2,	H0309: 2, H0457: 2,	H0178: 2, H0620: 2,	T0010: 2, H0083: 2,	S6028: 2, T0006: 2,	H0604: 2, H0180: 2,	H0598: 2, H0090: 2,	H0264: 2, L0775: 2,	L0375: 2, L0655: 2,
H0584: 5, L0157: 5	H0424: 5,	H0542: 5, S0049: 4,	H0150: 4,	H0135: 4,	H0522: 4,	L0439: 4,	H0423: 4,	H0656: 3,	H0619: 3,	T0042: 3,	S0002: 3,	L0761: 3,	L0659: 3,	H0422: 3,	H0650: 2,	H0645: 2,	H0156: 2,	H0309: 2,	H0178: 2,	T0010: 2,	S6028: 2,	H0604: 2,	H0598: 2	H0264: 2,	L0375: 2,
Ser-259,	Gly-302,																								
Gln-251 to Ser-259,	Arg-273 to Gly-302,	Lys-317 to Thr-349,	Ala-351 to Arg-368.							. •														٠	
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.0635: 2, L0663: 2,	H0697: 2, H0658: 2,	S0027: 2, L0740: 2,	3756:	H0445: 2, L0589: 2,	.0599; 2, H0170; 1	H0265: 1, H0295: 1	H0583: 1, H0341: 1	H0255: 1, H0459: 1	Н0638: 1, Н0637: 1	S0045: 1, S6026: 1	H0351: 1, S6016: 1,)222:	H0574: 1, H0486: 1	H0013: 1, H0250: 1	H0069: 1, H0075:	H0427: 1, H0042: 1	H0036: 1, H0004: 1	S0010: 1, T0048: 1	H0318: 1, H0434: 1	H0052: 1, H0086:	H0572: 1, H0123:	H0012: 1, H0024: 1	S0051: 1, H0594: 1	H0428: 1, H0031: 1,	H0165: 1, L0456: 1,
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AR089: 9, AR061: 7	H0040: 5, H0547: 5,	S0152: 5, L0593: 5,	L0595: 5, H0551: 4,	H0529: 4, H0519: 4,	H0560: 3, H0561: 3,	H0657: 2, S0360: 2,	S0007: 2, H0586: 2,	H0013: 2, H0494: 2,	L0809: 2, H0435: 2,	S0028: 2, L0748: 2,	L0439: 2, L0731: 2,	L0759: 2, H0445: 2,	L0592: 2, H0542: 2,	H0624: 1, H0170: 1,	H0556: 1, S0212: 1,	H0663: 1, S0418: 1,	S0356: 1, S0046: 1,	H0393: 1, H0486: 1,	H0427: 1, H0156: 1,	H0036: 1, H0318: 1,	T0110: 1, H0545: 1,	H0014: 1, H0266: 1,	H0188: 1, S0022: 1,	H0328: 1, H0688: 1,	T0023: 1, H0032: 1,
Arg-1 to Asn-7,	Leu-56 to Met-61.							-																	,
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H0038: 1, H0268: 1,	S0142: 1, S0422: 1,	S0426: 1, L0761: 1,	L0646: 1, L0765: 1,	L0773: 1, L0794: 1,	L0766: 1, L0804: 1,	L0776: 1, L0655: 1,	L0659: 1, L0791: 1,	L0792: 1, L0663: 1,	L0664: 1, H0666: 1,	H0672: 1, H0539: 1,	H0555: 1, L0743: 1,	L0740: 1, L0749: 1,	L0779: 1, L0752: 1,	S0026: 1, S0194: 1,	H0543: 1, H0423: 1 and	S0424: 1.	AR089: 2, AR061: 2	L0438: 12, L0439: 11,	H0617: 5, H0556: 4,	H0618: 3, H0253: 3,	L0769: 3, L0761: 3,	L0759: 3, H0544: 2,	H0031: 2, H0135: 2,	H0038: 2, H0641: 2,	L0764: 2, L0783: 2,
										•						-	Glu-6 to Gly-11,	Gly-64 to Ser-70,	Val-140 to Val-145,	His-163 to Leu-168,	Leu-189 to Lys-198,	Ser-221 to Thr-227,	His-261 to Pro-270.		
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L0809: 2, L0790: 2,	L0666: 2, L0663: 2,	L0665: 2, H0144: 2,	S0330; 2, L0751: 2,	L0779: 2, H0543: 2,	H0265: 1, H0685: 1,	H0657: 1, H0306: 1,	S0420: 1, S0354: 1,	S0360: 1, S0046: 1,	L0717: 1, H0550: 1,	H0592: 1, H0333: 1,	H0331: 1, H0559: 1,	H0486: 1, H0013: 1,	H0244: 1, H0635: 1,	H0575: 1, H0596: 1,	T0110: 1, H0123: 1,	H0615: 1, H0033: 1,	H0553: 1, H0212: 1,	H0124: 1, H0040: 1,	H0616: 1, H0264: 1,	H0488: 1, H0100: 1,	H0494: 1, H0131: 1,	H0529: 1, L0637: 1,	L0772: 1, L0766: 1,	L0775: 1, L0375: 1,	L0776: 1, L0628: 1,
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	Trp-22 to Glu-35.		Met-1 to Tyr-14,	Arg-24 to Gly-30,	His-49 to Cys-55,	Ile-94 to Phe-99,	Pro-128 to Gly-136.	Glu-1 to Thr-6.								
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				His-15 to Ser-21,	Asp-44 to Val-65,	Glu-95 to Thr-101,	Ala-131 to Asp-142.	-	Ser-28 to Glu-34,	Ser-77 to Arg-82,	Trp-127 to Arg-135.				•										
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S0392: 1, L0750: 1 and L0777: 1	AR089: 13, AR061: 3 H0529: 1 and H0693:					•	AR089: 2, AR061: 2	H0521: 2, L0759: 2,	H0341: I, H0620: 1,	H0266: I and L0766: 1.	AR061: 6, AR089: 3	H0622: 2, H0253: 1	and S0152: 1.	AR089: 1, AR061: 0	L0766: 5, L0806: 3,	T0010: 2, L0761: 2,	H0521: 2, L0752: 2,	H0677: 2, S0278: 1,	H0559: 1, H0486: 1,	H0427: 1, S0038: 1,	L0796: 1, L0644: 1,	L0771: 1, L0659: 1,	L0666: 1, L0664: 1,
	Gly-42 to Ser-48.		` .				Ser-18 to Ile-27,	Asp-124 to Gln-138.	,		Pro-25 to Ala-34,	Ser-69 to Ala-74,	Glu-92 to Gly-98.	Ser-7 to Asp-13.		¥ .							
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L0779: 1, H0445: 1 and	L0595: 1.	AR089: 23, AR061: 14 17q23-q24	H0208: 1 and H0290:															AR061: 3, AR089: 2	H0038: 4, L0748: 4,	S0222: 2, L0598: 2,	L0776: 2, L0439: 2,	L0780: 2, L0752: 2,	H0050: 1, T0006: 1,	H0111: 1, S0036: 1,	H0616: 1, T0067: 1,
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	,												·	Ser-1 to Gly-7,	Asp-24 to Leu-31,	Lys-50 to Arg-58,	Glu-65 to Arg-73,	Thr-102 to His-109,	Arg-116 to Ile-122.	Ala-11 to Gln-16,	Leu-46 to Ala-52;	Gln-84 to Glu-89,	Phe-105 to Ser-111.		
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L0368: 1, S0052: 1,	S0146: 1, S0390: 1,	S0028: 1 and S0260: 1.	AR061: 1, AR089: 0	L0439: 4, H0543: 3,	S0360: 2, L0662: 2,	L0742: 2, L0481: 1,	H0619: 1, H0486: 1,	L0586: 1, L0021: 1,	S0051: 1, H0424: 1,	L0789: 1, S0374: 1,	H0539: 1, L0744: 1,	L0754: 1, L0777: 1,	L0752: 1 and H0506: 1.	AR089: 3, AR061: 1	H0624: 2, S0356: 1,	H0607: 1, L0060: 1 and	H0506: 1.			,	AR051: 10, AR054:	10, AR050: 9, AR089:	5, AR061: 3	L0775: 4, H0046: 3,	H0622: 3, H0660: 3,
			Thr-6 to Tyr-13,	Ala-23 to Asp-30,	Phe-66 to Arg-71,	Pro-92 to Glu-102,	Arg-108 to Leu-116,	Tyr-159 to Thr-164.		,				Leu-8 to Pro-14,	Pro-59 to Asn-64,	Pro-80 to Glu-91,	Gly-127 to Lys-134,	Arg-146 to Glu-152,	Thr-156 to Asp-165,	Pro-184 to Asp-203.	Arg-1 to Gly-8,	Gly-10 to Leu-17,	Lys-41 to Pro-51,	Lys-67 to Thr-74,	Glu-94 to Lys-99,
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Phe-107 to Gly-112,	Arg-125 to Glu-131,	Leu-141 to Arg-153,	Gly-168 to Ala-176,	Asn-210 to Arg-215,	Asn-222 to Ser-234,	Leu-238 to Thr-249.	•			,							:	Arg-14 to Glu-20,	Leu-30 to Arg-42,	Gly-57 to Ala-65,	Asn-99 to Arg-104,	Asn-111 to Ser-117.			
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																	÷					Ser-12 to Ser-19,	Ser-34 to Lys-47.		Phe-40 to Tyr-47,
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13, AR089: 3, AR061: 2	L0731: 4, L0596: 4,	H0615: 3, L0777: 3,	H0625: 2, L0803: 2,	L0740: 2, H0657: 1,	H0393: 1, H0441: 1,	F0109: 1, H0318: 1,	H0581: 1, H0566: 1,	H0551: 1, L0761: 1,	L0641: 1, L0766: 1,	L0650: 1, L0784: 1,	H0144: 1, H0547: 1,	H0539: 1, H0696: 1,	S3014: 1, L0744: 1,	L0779: 1 and L0780: 1.	AR089: 19, AR061: 7	L0771: 4, L0764: 3,	H0282: 2, H0494: 2,	L0518: 2, L0617: 1,	L0794: 1, L0774: 1,	.0806: 1, L0657: 1,	L0663: 1, S0374: 1,	H0672: 1, L0752: 1 and	55: 1.	AR089: 0, AR061: 0
13, 4		90H	H06	T027	H03	T01(H05	H05	7907	F06	10H	H05.	S301	L077	ARO		H028	L051	L07	0807	F066	.90H	L0755: 1	ARO
lle-119 to Arg-125, Ser-141 to Arg-200,	Arg-217 to Lys-223,	Ala-303 to Leu-311.							,	·														Tyr-11 to Val-16,
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5: 15,	: 5, LO	5, S0	3, H0	: 3, H(. 2, SO	2, H0	2, L0	2, L0	2, HC	2, L0	2, S0 ²	1, HC	1, S0	1, S0	1, H0	1, H0	1, H0	1, H0	1, H0	1, S0(1, H0	1, H0	1, H0	1, S0	1, H0
T076	H0659: 5, L0749: 5,	L0759: 5, S0374: 4,	L0804: 3, H0547: 3,	H0658: 3, H0170: 2,	H0650: 2, S0418: 2,	S0280: 2, H0598: 2,	.0763: 2, L0803: 2,	.0666: 2, L0663: 2,	H0435: 2, H0660: 2,	L0748: 2, L0757: 2,	S0026: 2, S0424: 2,	H0686: 1, H0657: 1,	H0662: 1, S0420: 1,	S0358: 1, S0376: 1,	C0717: 1, H0574:	H0486: 1, H0596: 1	_0471: 1, H0024:]	H0014: 1, H0083: 1	H0510: 1, H0266: 1	S0250: 1, S0003: 1	H0428: 1, H0032:	H0591: 1, H0040:	H0634: 1, H0616: 1	H0560: 1, S0440: 1,	H0641: 1, H0529:
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Glu-37 to Arg-42,	Asn-50 to Arg-58,	Leu-82 to Leu-96,	Glu-112 to Gln-120.							•			*												
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	Trp-3 to Thr-14,	Ala-21 to Arg-30,	Glu-66 to Pro-74,	Pro-103 to Gly-108,	Ile-135 to Ile-142.									Ala-18 to Arg-23,	Gly-28 to Trp-35,	Gln-53 to Arg-61,	Asp-122 to Glu-127,	Gln-163 to Cys-171.				Gly-35 to Asp-41.	-		
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H0521: 2, L0756: 2,	L0731: 2, L0758: 2,	L0588: 2, H0556: 1,	S0282: 1, H0662: 1,	H0402: 1, S0418: 1,	Т0008: 1, S0222: 1,	H0392: 1, H0333: 1,	L0021: 1, H0581: 1,	S0049: 1, L0471: 1,	H0266: 1, L0351: 1,	L0772: 1, L0766: 1,	L0776: 1, L0659: 1,	L0792: 1, H0522: 1,	S0027: 1, L0779: 1 and	S0011: 1.	AR089: 1, AR061: 1	L0759: 2, H0171: 1,	T0010: 1, H0090: 1,	L0761: 1, L0766: 1,	S3014: 1, L0745: 1,	L0747: 1 and H0506: 1.		AR089: 3, AR061: 1	S0354: 1 and H0030: 1.		
										٠,				,		•						Glu-7 to Gln-17,	Tyr-27 to Cys-32,	Thr-63 to Lys-70,	Glu-89 to Lys-94,
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		AR061: 3, AR089: 0	S0001: 1, H0619: 1 and	H0521: 1.	AR089: 1, AR061: 0	L0789: 4, H0539: 4,	L0731: 4, H0052: 3,	L0779: 3, S0007: 2,	L0157: 2, H0123: 2,	H0233: 2, L0637: 2,	80356: 1, 80360: 1,	H0550: 1, H0486: 1,	H0013: 1, H0253: 1,	H0620: 1, H0408: 1,	H0188: 1, S0250: 1,	L0193: 1, L0455: 1,	H0135: 1, H0551: 1,	L0770: 1, L0794: 1,	L0776: 1, L0665: 1,	S0392: 1, L0750: 1 and	L0777: 1.	AR089: 16, AR061: 11	L0789: 4, L0731: 4,	H0539: 3, L0779: 3,	S0007: 2, H0052: 2,
Tyr-100 to Ser-107,	Lys-122 to Val-127.			-	Glu-47 to Asp-56,	Tyr-131 to Gly-136.				,												Glu-48 to Asp-57.		ı	
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L0157: 2, H0123: 2,	H0233: 2, L0637: 2,	S0356: 1, S0360: 1,	H0550: 1, H0253: 1,	H0620: 1, H0408: 1,	H0188: 1, S0250: 1,	L0193: 1, L0455: 1,	H0135: 1, H0551: 1,	L0770: 1, L0794: 1,	L0776: 1, L0665: 1,	S0392: 1, L0750: 1 and	L0777: 1.	AR061: 5, AR089: 2	H0521: 4, H0457: 3,	H0580: 2, L0749: 2,	L0588: 2, H0556: 1,	H0485: 1, H0635: 1,	H0581: 1, H0251: 1,	H0124: 1, H0551: 1,	H0529: 1, L0667: 1,	L0773: 1, L0803: 1,	S0052: 1, H0593: 1 and	50424: 1.	AR089: 0, AR061: 0	H0494: 1, H0520: 1,	H0435: 1 and H0423: 1.
									`	,		Arg-1 to Ser-6,	Asn-55 to Phe-64,	Ser-86 to Gly-92,	Leu-124 to Glu-146.							-	Gln-12 to Pro-20,	Thr-37 to Glu-42,	Ile-49 to Arg-56,
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						-						2 - 628						•					1 - 447		
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,							108725,	120700,	133171,	136836,	145981,	147141,	164953,	188070,	600957,	601238,	601846,	602216,	602477					,	
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		AR061: 2, AR089: 2	L0439: 2, L0617: 1,	S0356: 1, H0457: 1,	S0036: 1, H0547: 1,	L0758: 1 and L0608: 1.	AR089: 14, AR061: 4	H0436: 11, H0255: 7,	H0559: 7, H0521: 7,	H0254: 4, H0423: 4,	H0265: 3, H0486: 3,	H0250: 3, H0581: 3,	H0271: 3, H0124: 3,	H0264: 3, H0555: 3,	H0341: 2, S0354: 2,	H0580: 2, H0370: 2,	H0586: 2, H0257: 2,	H0069: 2, H0083: 2,	H0031: 2, H0634: 2,	H0488: 2, S0422: 2,	S0426: 2, L0766: 2,	L0649: 2, L0805: 2,	L0653: 2, L0776: 2,	L0655: 2, L0731: 2,	H0445: 2, H0543: 2,
Leu-75 to Arg-88,	Ala-111 to Leu-118.	Arg-75 to Lys-83,	Ser-89 to Arg-102,	Met-136 to Arg-142.	-		Ala-89 to Glu-98,	Leu-117 to Ala-123,	Glu-139 to Gly-147,	Leu-158 to Thr-163,	Glu-195 to Arg-211.							,							
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H0677: 2, H0556: 1, H0584: 1, H0140: 1,	H0583: 1, H0656: 1, H0402: 1, H0305: 1,	H0458: 1, S0140: 1,	H0550: 1, H0497: 1,	H0575: 1, S0474: 1,	H0421: 1, H0024: 1,	H0213: 1, H0087: 1,	H0272: 1, H0641: 1,	S0144: 1, L0763: 1,	.0761: 1, L0662: 1,	 L0804: 1, L0659: 1,	.0787: 1, L0666: 1,	.0663: 1, H0518: 1,	S0044: 1, H0576: 1,	L0756: 1, H0422: 1,	S0452: 1 and H0506: 1.	AR061: 2, AR089: 1						
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						Lys-12 to Pro-22,	Lys-38 to Thr-45,	Glu-65 to Lys-70,	Phe-78 to Gly-83,	Arg-96 to Glu-102,	Leu-112 to Arg-124,	Gly-139 to Ala-147,	Asn-181 to Arg-186,	Asn-193 to Ser-205,	Leu-209 to Thr-220.				,						
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.0777: 2, S0026: 2,	H0583: 1, S0282: 1,	H0305: 1, S0356: 1,	S0358: 1, S0045: 1,	S0046: 1, H0619: 1,	H0485: 1, S0280: 1,	H0042: 1, H0569; 1,	.0024: 1, H0051: 1,	.0071: 1, H0355: 1,	H0510: 1, H0328: 1,	H0615: 1, H0428: 1,	H0030: 1, L0142: 1,	S0364: 1, H0361: 1,	H0040: 1, H0413: 1,	H0059: 1, S0038: 1,	.0763: 1, L0770: 1,		0644: 1, L0363: 1,	L0806: 1, L0657: 1,	0783: 1, L0809: 1,	.0664: 1, H0519: 1,	H0690: 1, H0670: 1,	H0672: 1, S0146: 1,	H0555: 1, H0479: 1,	S3012: 1, S0028: 1,	L0779: 1, L0731: 1,
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		-				Pro-1 to Met-7,	Ala-16 to Gly-24,	Gly-26 to Leu-33,	Lys-57 to Pro-67,	Lys-83 to Thr-90,	Glu-110 to Lys-115,	Phe-123 to Gly-128,	Arg-141 to Glu-147,	Leu-157 to Arg-169,	Gly-184 to Ala-192,	Asn-226 to Arg-231,	Asn-238 to Ser-250,	Leu-254 to Thr-265.								
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S0424: 1.	AR061: 4, AR089: 2	H0622: 2, S0212: 1,	H0253: 1, S0152: 1,	L0748: 1, L0603: 1 and	H0668: 1.	AR089: 104, AR061:		S0278: 4, H0581: 4,	L0751: 4, H0620: 3,	L0764: 3, L0662: 3,	L0659: 3, L0439: 3,	L0754: 3, H0542: 3,	H0170: 2, H0402: 2,	H0580: 2, H0550: 2,	H0333: 2, H0012: 2,	T0010: 2, H0252: 2,	H0063: 2, H0059: 2,	S0002: 2, L0775: 2,	L0655: 2, L0663: 2,	L0665: 2, H0593: 2,	H0658: 2, H0539: 2,	H0555: 2, L0743: 2,	L0744: 2, L0752: 2,	L0731: 2, H0543: 2,	H0624: 1, H0265: 1,
						Gln-15 to Asp-21,	Leu-40 to Asp-47,	Gly-70 to Leu-84,	Leu-88 to Arg-93,	Lys-98 to Asp-105,	Glu-136 to Arg-148,	Thr-197 to Ala-204,	Asp-222 to Glu-232,	Glu-261 to Gln-269,	Arg-295 to Trp-300,	Asn-306 to Pro-314,	Lys-395 to Lys-415.		_					,	
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H0650: 1, H0656: 1	S0212: 1, H0306: 1	H0305: 1, S0360: 1	S0046: 1, H0619: 1	S0222: 1, S6014:	0613: 1, H049	H0250: 1, H0635: 1	H0427: 1, L0021:	H0036: 1, H0421:	H0399: 1, H0416:	0188: 1, S025	L0143: 1, H0617: 1,	H0673: 1, H0124:	H0163: 1, H0634:	H0087: 1, T0067:	H0264: 1, H0272:	H0412: 1, H0413:	H0100: 1, S0344: 1	S0426: 1, L0770: 1	L0638: 1, L0761: 1	.0794: 1, L0650:	L0661: 1, L0546: 1	S0053: 1, H0689: 1	H0521: 1, S3014: 1	L0748: 1, L0740: 1	L0779: 1, L0780: 1
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L0753: 1, L0759: 1,	H0445: 1, H0595: 1,	L0362: 1, H0653: 1 and	H0506: 1.	AR061: 3, AR089: 2	L0741: 12, L0744: 6,	H0052: 5, H0040: 5,	L0742: 5, L0748: 5,	H0620: 4, L0794: 4,	H0486: 3, H0622: 3,	L0439: 3, L0749: 3,	_0777: 3, S0354: 2,	H0046; 2, H0031: 2,	H0617: 2, L0770: 2,	L0761: 2, L0806: 2,	S0126: 2, H0539: 2,	H0518: 2, H0521: 2,	L0751: 2, L0747: 2,	L0758: 2, L0593: 2,	H0624: 1, H0171: 1,	S0114: 1, H0650: 1,	S0418: 1, S0420: 1,	H0645: 1, H0351: 1,	H0370: 1, H0600: 1,	H0592: 1, L0622: 1,	F0082: 1, S0474: 1,
				Arg-11 to Arg-19,	Ser-36 to Thr-61,		Ala-100 to Gln-106,	Ser-155 to Leu-161.							91	I		Notice of the control			<u> </u>	Nanhord .			
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H0085: 1, H0235: 1, H0545: 1, H0012: 1, H0644: 1, H0124: 1, H0634: 1, H0494: 1,	S0144: 1, S0142: 1, L0638: 1, L0642: 1, L0764: 1, L0771: 1,	L0649: 1, L0774: 1, L0775: 1, L0651: 1, L0653: 1, L0776: 1,	L0659: 1, L0809: 1, S0374: 1, H0690: 1,	H0522: 1, H0696: 1, L0740: 1, L0754: 1, L0755: 1, L0731: 1,	L0757: 1, H0707: 1, L0601: 1 and H0543: 1.	AR054: 26, AR051: 12, AR050: 10, AR061:	/, AR089: 4 H0556: 4, L0770: 4, L0794: 4, L0758: 4,	L0731: 3, H0038: 2, L0766: 2, L0659: 2, S0212: 1, S0132: 1,
		·				Arg-41 to Thr-53, Ser-89 to Glu-95,	Len-109 to Lys-114, Pro-189 to Glu-194.	
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H0632: 1, H0618: 1, H0271: 1, S0368: 1, H0673: 1, L0667: 1, L0662: 1, L0767: 1, L0768: 1, L0381: 1,	L0789: 1, L0790: 1, L0664: 1, L0665: 1, H0659: 1, H0658: 1,	S0328: 1, S0454: 1, L0749: 1, L0777: 1, H0542: 1 and H0677: 1.	AR089: 1, AR061: 0 H0642: 2 and S0053: 1.	AR089: 16, AR061: 6 H0144: 6, H0013: 2 and S0356: 1.	•	AR089: 17, AR061: 13 S0049: 1, H0144: 1 and L0439: 1.	AR061: 1, AR089: 0 L0748: 7, L0766: 6, L0756: 5, H0580: 4, L0777: 3, H0052: 2,
		,	Asn-48 to Gly-54, Thr-56 to Lys-69.	Gly-1 to Val-11, Gly-50 to Thr-62, Asn-125 to Gly-132, Leu-172 to Asn-178	Ser-210 to Ser-217, Ser-232 to Lys-245.	Leu-21 to Asp-33.	Gln-36 to Thr-42, Glu-99 to Leu-104.
			1032	1033		1034	1035
			30 - 653	2 - 799		1 - 714	16 - 438
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S0051: 2, H0644: 2,	H0551: 2, L0769: 2,	H0144: 2, L0743: 2,	.0754: 2, L0779: 2, .	.0755: 2, L0759: 2,	H0657: 1, H0656: 1,	S0116: 1, H0341: 1,	S0212: 1, S0282: 1,	H0125: 1, L0005: 1,	S0222: 1, H0431: 1,	H0438: 1, H0586: 1,	Н0069: 1, Н0635: 1,	.0157: 1, H0050: 1,	.0471: 1, H0051: 1,	H0399: 1, H0375: 1,	S0318: 1, S0316: 1,	H0687: 1, S0250: 1,	H0031: 1, H0553: 1,	H0090: 1, H0634: 1,	H0616: 1, H0623: 1,	S0038: 1, H0100: 1,	.0371: 1, L0667: 1,	.0800: 1, L0794: 1,	.0804: 1, L0775: 1,	.0805: 1, L0776: 1,): 1, L0526: 1,
S0051	H055	H014	L0754	L0755	H0657	S0116	S0212	H012	S0222	H0438	900H	L0157	L0471	H039	80318	.890H	H003	H009(H0616	8003	L0371)080T	T0807	T0805	L0659: 1
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L0792: 1, L0663: 1, L0438: 1, H0547: 1, S0126: 1, L0439: 1, L0740: 1, L0749: 1, L0752: 1, S0031: 1, H0445: 1, L0480: 1, L0604: 1, S0026: 1, H0542: 1, S0412: 1 and H0352: 1.	AR089: 12, AR061: 6	H0575: 1, H0271: 1	and H0521: 1.								AR061: 3, AR089: 2	S0007: 3, S0001: 1,	H0618: 1, H0009: 1,	S0051: 1, L0763: 1,	L0439: 1 and L0758: 1.		AR089: 14, AR061: 6
	Glu-8 to Pro-17,	Pro-31 to Asp-37.			-						Ser-12 to Gln-25,	Pro-29 to Phe-39,	Gly-81 to Gly-89,	Glu-143 to Trp-156.		Arg-82 to Trp-88.	Pro-17 to Asn-23.
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	S0300: 2, L0439: 2,	H0438: 1, H0618: 1,	H0052: 1, H0616: 1,	H0488: 1, L0772: 1,	L0806: 1, L0384: 1,	L0666: 1, L0758: 1 and	H0423: 1.	AR089: 1, AR061: 0	H0255: 2, H0486: 1,	H0581: 1, H0529: 1 and	H0543: 1.	•	AR061: 2, AR089: 1	H0586: 5, L0751: 2,	H0170: 1, H0638: 1,	H0553: 1, H0477: 1,	S0002: 1, H0529: 1,	L0766: 1, L0803: 1,	H0672: 1 and H0543: 1.	AR089: 2, AR061: 1	H0521: 4, L0803: 3,	S0358: 2, H0489: 2,	H0046: 2, L0794: 2,	L0666: 2, H0144: 2,	S0126: 2, S0342: 1,	H0663: 1, S0356: 1,
								Asp-2 to Pro-7,	Leu-18 to Arg-27,	Glu-52 to Ser-59,	Pro-90 to Pro-97,	Pro-116 to Glu-121.	Ala-1 to Arg-9,	Leu-11 to Pro-18.						Arg-9 to Arg-18,	Leu-107 to Gln-113,	Asp-126 to Thr-131.				
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H0013: 1, L0021: 1,	H0705: 1, H0150: 1,	H0266: 1, H0039: 1,	H0622: 1, H0038: 1,	H0551: 1, S0422: 1,	L0598: 1, L0646: 1,	L0766: 1, L0653: 1,	L0656: 1, L0789: 1,	L0532: 1, L0663: 1,	H0658: 1, L0748: 1,	L0759: 1, S0434: 1,	L0596: 1 and H0506: 1.	AR061: 2, AR089: 2	L0439: 11, L0794: 5,	L0666: 5, S0222: 4,	H0052: 3, L0756: 3,	H0624: 2, S6028: 2,	S0038: 2, L0638: 2,	L0805: 2, L0664: 2,	L0438: 2, L0740: 2,	H0171: 1, S6024: 1,	H0013: 1, H0374: 1,	H0050: 1, S0050: 1,	H0051: 1, S0386: 1,	L0769: 1, L0768: 1,	L0776: 1, L0659: 1,
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L0789: 1, H0144: 1,	L0745: 1 and L0746: 1.	AR089: 3, AR061: 1	H0271: 10, H0052: 8,	H0556: 7, L0439: 7,	L0754: 7, H0622: 6,	L0776: 5, L0769: 4,	H0265: 3, H0295: 3,	H0580: 3, S0222: 3,	H0013: 3, H0156: 3,	H0051: 3, H0494: 3,	L0659: 3, S0356: 2,	H0208: 2, S6014: 2,	H0135: 2, H0634: 2,	S0002: 2, S0426: 2,	L0770: 2, L0796: 2,	L0373: 2, L0803: 2,	L0375: 2, L0655: 2,	L0666: 2, L0438: 2,	H0672: 2, H0521: 2,	L0747: 2, L0750: 2,	L0756: 2, L0588: 2,	H0542: 2, H0543: 2,	H0170: 1, S0212: 1,	S0282: 1, S0030: 1,	H0305: 1, H0589: 1,
		Tyr-41 to Leu-52,	Leu-64 to Cys-72,	Pro-92 to Arg-98,	Ser-110 to Glu-116.					,			-												
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1 110610: 1	[L0619: 1, f10019: 1,	S6026: 1, H0550: 1,	H0370: 1, H0600: 1,	H0592: 1, H0486: 1,	Т0040: 1, Н0635: 1,	H0002: 1, S0010: 1,	H0390: 1, H0581: 1,	H0421: 1, H0085: 1,	T0110: 1, H0041: 1,	N0006: 1, H0050: 1,	H0012: 1, H0620: 1,	T0003: 1, H0024: 1,	H0687: 1, H0252: 1,	H0604: 1, H0031: 1,	H0644: 1, H0628: 1,	H0598: 1, H0087: 1,	H0264: 1, S0112: 1,	Т0041: 1, Н0560: 1,	S0150: 1, H0529: 1,	L0640: 1, L0761: 1,	L0643: 1, L0806: 1,	L0658: 1, L0809: 1,	L0544: 1, L0788: 1,	L0663: 1, L0664: 1,	L0665: 1, S0428: 1,	S0053: 1, H0144: 1,
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70701)690H	H057	L074(10759	L059	990H			H065	8027	H062	H027	8014	H059				790H	990T	H05				H03	ARO	l
							Gly-18 to His-25.	,							Leu-13 to Val-25,	His-32 to Arg-39.					Gln-7 to Asp-19,	Leu-34 to Ser-42.				
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							641 - 1756								316 - 567					-	194 - 616				2-637	
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S0136: 3, L0779: 3,	H0171: 1, H0052: 1,	H0038: 1, L0766: 1,	H0547: 1, S0031: 1 and	S0242: 1.	AR089: 26, AR061: 4	S0354: 1, H0561: 1 and	L0603: 1.	AR061: 49, AR089: 19	AR061: 2, AR089: 1	L0766: 2, S0001: 1,	H0592: 1, H0575: 1,	H0644: 1, H0038: 1 and	H0144: 1.	AR089: 1, AR061: 0	H0638: 2, H0521: 2,	L0752: 2, H0677: 2,	H0650: 1, H0484: 1,	H0458: 1, H0580: 1,	H0586: 1, H0575: 1,	H0081: 1, S0036: 1,	H0063: 1, H0560: 1,	L0809: 1, S0126: 1,	S0328: 1, L0744: 1,	L0740: 1, L0754: 1 and
			-		Ile-44 to Gln-50.		-	Asp-1 to Pro-12.	Glu-18 to Thr-23.								-					-		
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H0543: 1.	AR054: 23, AR050:	18, AR051: 12, AR061:	12, AR089: 8	L0803: 7, L0794: 4,	L0748: 4, L0591: 4,	L0770: 3, L0804: 3,	S0142: 2, L0789: 2,	L0743: 2, L0747: 2,	L0749: 2, L0752: 2,	S0360: 1, S0046: 1,	H0549: 1, H0309: 1,	H0327: 1, H0012: 1,	L0769: 1, L0773: 1,	L0767: 1, L0774: 1,	L0775: 1, L0776: 1,	L0790: 1, L0791: 1,	H0435: 1, H0660: 1,	H0648: 1, H0521: 1,	H0555: 1, L0750: 1,	L0779: 1, L0777: 1,	L0755: 1, L0758: 1 and	S0434: 1.	AR089: 1, AR061: 0	L0766: 7, H0486: 4,	L0794: 4, H0520: 4,
	Glu-25 to Arg-31,	Glu-71 to His-76,	Leu-85 to Leu-92,	Gly-129 to Ser-143.				·		*.											.,				
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L0754: 4, L0777: 4,	.0755: 4, L0599: 4,	.0803: 3, L0779: 3,	H0542: 3, H0624: 2,	S0418: 2, S0360: 2,	H0551: 2, L0770: 2,	.0662: 2, L0558: 2,		H0547: 2, H0519: 2,	H0522: 2, L0756: 2,	L0758: 2, L0588: 2,	H0170: 1, H0556: 1	H0657: 1, H0580: 1	_0717: 1, S0222:	H0574: 1, H0599:	S0474: 1, H0544:	H0266: 1, H0252:	F0023: 1, H0553:	F0042: 1, S0422:	_0369: 1, L0763:	.0761: 1, L0772:	L0521: 1, L0387: 4	.0650: 1, L0806:		L0789: 1, L0790: 1	L0663: 1, S0053: 1
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S0374: 1, H0435:	H0670: 1, H0651:	H0521: 1, H0436:	H0345: 1, L0439:		.0750: 1, L0759:	.0485: 1, L0593:	S0026: 1, H0665:	H04	ind 9	1, A	,10	H03	L07	H05	H04	90H	H01	90H	L07) H06	L0785: 1, H0341:	H04	S0420: 1, H0580:	90H	H0550: 1, S0222:
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L0163: 4, L0777: 4,	L0520: 3, H0002: 2,	S0364: 2, S0330: 2,	L0747: 2, H0171: 1,	H0549: 1, H0486: 1,	H0013: 1, H0253: 1,	H0318: 1, S0049: 1,	H0251: 1, L0471: 1,	S0051: 1, H0616: 1,	S0038: 1, H0100: 1,	H0561: 1, L0803: 1,	L0782: 1, L0809: 1,	L0779: 1, L0759: 1 and	L0584: 1.			
					,							,		1236 His-10 to Gly-16,	Pro-65 to Ala-70,	Ala-96 to Lys-101.
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- [51] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.
- The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.
- [53] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.
- [54] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

Column 8 in Table 1A provides an expression profile and library code: count for [55] each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove nonspecific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalizé gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[56] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more

sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[57] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIMTM (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID	SEQ ID	CONTIG	BAC ID: A	SEQ ID NO:B	EXON From-To
NO:Z	NO:X	ID:	A CO69206	1268	1-225
HFCBB56	24	910073	AC068296		1-70
HIBBF63	75	912715 •	AC009065	1269	850-1112
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					1707-1779
					i la
					1874-1924
		'		·	2836-2908
					3006-4160
HIBBF63	75	912715	AC012171	1270	1-64
	•				159-209
	*	131			1122-1194
					1292-1527
				· · · · · · · · · · · · · · · · · · ·	1593-2446
HIBBF63	75	912715	AC005346	1271	1-70
·					874-1136
					1193-1646
		,			1731-1803
		1.	_		1898-1948
		-			2861-2933
					3031-4185
HIBBF63	75	912715	AC009065	1272	1-547
HIBBF63	75	912715	AC012171	1273	1-547
HIBBF63	75	912715	AC009065	1274	1-424
HIBBF63	75	912715	AC005346	1275	1-547
HIBBF63	75	912715	AC012171	1276	1-419
HIBBF63	75	912715	AC005346	1277	1-424
H2CBH45	90	963811	AC068243	1278	1-267
MZCBITIS					1540-1640
				-	3095-3380
					3393-3556
					3901-3967
					4137-4639
					5287-5856
					5916-6588
					7029-7876
					8324-8414
U2CDU45	90	963811	AC068243	1279	1-309
H2CBH45 HBGQT03	93	908173	AC024045	1280	1-218

					457-549
	·				660-819
					2039-2238
ļ					2529-2763
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					4184-4322
•					4727-4851
					5161-6181
HBGQT03	93	908173	AC024045	1281	1-176
HBGQT03	93	908173	AC024045	1282	1-461
COTODAN	93	, , , , , , , , , , , , , , , , , , , ,		-	960-1030
				·	1194-1959
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			-		5321-5461
					6521-7174
					7564-7841
			-		8311-8758
					8829-8969
				,	8997-10118
					10257-10910
				. 80	12058-12385
					12438-12953
			-		13729-13873
НСЕРН71	97	522739	AL365319	1283	1-494
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					1584-1839
					2455-2586
					2689-2787
HFKHR40	431	952470	AC018805	1503	1-525
	1 .				612-1372
		1	,	,	

,					1732-2155
					2345-2460
		·			2652-3025
					3157-3251
					3449-3540
					3680-3780
					3914-4131
			-		4215-4491
					4603-4741
					4913-4987
					5135-5190
]	ļ		5435-5571
					5901-6011
					6309-6423
					6922-8294
					8370-8522
HFKHR40	431	952470	AC061707	1504	. 1-527
			. *		614-1374
					1478-1732
	ļ				1734-2158
					2348-2463
		-			2655-3027
					3159-3253
					3451-3542
			-		3682-3782
					3916-4134
	1			,	4219-4495
					4607-4745
				-	4917-4991
				1	5139-5194
					5439-5575
					5905-6015
					6313-6427
					6926-9300
				}	9919-9960
					10029-10186
					11393-11624
					12094-12294
					13227-13375
					13690-13829

					14362-14486
HFKHR40	431	952470	AC018805	1505	1-343
					700-770
HFKHR40	431	952470	AC061707	1506	1-343
				1	700-771
HFKHR40	431	952470	AC061707	1507	1-277
HWLHF10	435	963422	AC010545	1508	1-40
					1661-1891
	<u> </u> -			1	2119-2199
					5160-5349
		·			6239-6607
			ļ		7675-8566
]	9450-9516
					9675-9752
		Ì			10110-10274
					14154-15055
					16384-16500
					17055-17139
					19941-20453
		,			20703-21216
					21806-21945
					23638-24171
		·			24527-24795
					25564-25656
-					26644-26787
					27284-27438
		į			28354-28612
					29247-29591
					29597-30208
					32018-32539
					33187-33942
HWLHF10	435	963422	AC010545	1509	1-721
HWLHF10	435	963422	AC010545	1510	1-610
				1.	675-1454
,					1591-2267
					2801-3363

Table 1B summarizes additional polynucleotides encompassed by the invention [59] (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

						70	NT From	NT TO
Clone ID	Contig ID:	SEQ ID	Analysis	PFam/NR Description	Pram/NR Accession Number	Percent		
Z:ON		NO:X	Method			Identity	-	
1 COTTO	1165061	=	blacty 14	(AB018414) Gab2 [Mus	gi 4589377 dbj BAA7	74%	51	227
HDP1E21	1000011	-	Didaka. 1 1	, incoming	6738.11	20%	246	416
				Illusculus		55%	1650	1784
						%59	1344	1421
			,			%89	1620	1991
						%69	1188	1226
			,			%99	1260	1295
				,		39%	1527	1595
	٠					32%	1017	1100
				,		45%	1182	1241
			*			36%	1528	1584
						34%	2907	2984
HDPTE21	887711	443	HMMER	PFAM: PH domain	PF00169	25.2	31	129
			2.1.1	PRINT PIT J. CO.	DE00160	80.9	664	156
H6EDR51	930788	445	HMMER	PFAM: PH domain	rrouto?			
			2.1.1 bloctv 7	(AF053974) SWAP-70	gb AAC40155.1	53%		966
			Diastx.2	[Mus musculus]	- 0	57%	1291	1395
						26%	1464	1760
						19%	1566	
						43%		
					Ž	33%	12	
HAPRA41	1154054	13	blastx.14	actin filament-associated	gi 487418 gb AAA18	82%	. 23	1261
				protein Canus ganus	DE00160	8 65	111	398
HAPRA41	926285	446	HMMER	PFAM: PH domain	rround			
_	_							

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473		484	759	727	771	1232	80	1316	396	1348	448	1	278		258		270			1343		1343		418		931			873
45		164	011	119	684	1062		402	13	1295	146		30		139		7					825		194		92	4		421
76%		33.2	1000/	0.001	92%	55.89	-	.65%	87%	77%	50.5		36%		44.9		37%			235.1		37%		85.1		100%			96%
gb AAA18166.1		PF00169	171 411 0520171 4 411	gb AAF185/2.1 AF1	01054 1	PF00018		emb CAB69447.1		-	PF00169		gi 5733602 gb AAD4 9698 114F163255 1		PF00169		gb AAD49698.1 AF1	63255_1		PF00620		emb CAA71241.1		PF00017		gb AAD49697.1 AF1	63254_1		pir T13601 T13601
actin filament-associated	protein [Gallus gallus]	PFAM: PH domain	· CLIC CO CO CO	(AF101054) PHR1	isoform 2 [Homo sapiens]	PFAM: Src homology	domain 3	unnamed protein product	funidentified		PFAM: PH (pleckstrin	homology) domain	(AF163255) adaptor	musculus]	PFAM: PH domain		(AF163255) adaptor	protein DAPP1 [Mus	musculus]	PFAM: RhoGAP domain	,	racGAP [Dictyostelium	discoideum]	PFAM: Src homology	domain 2	(AF163254) adaptor	protein DAPP1 [Homo	sapiens]	hypothetical protein
blastx.2		HMMER 2 1 1	7.1.1	blastx.2		HMMER		-			HMMER	8.1	blastx.14		HMMER	2.1.1	blastx.2			HMMER	2.1.1	blastx.2		HMMER	2.1.1	blastx.2			blastx.14
-	-	447				15					448		17		449			′		18				19					20
		954118				910086					860196		1150868		927873					006606	·			962403					1228284
		HBXBI07				HBXCM38					HCE3E50		НСЕОДО4		НСЕОДО04					HDPHI92				HDPLT89					HDPSU48

485	898	000	862			COL	708		756					1507	533		629	514	+ 10	595		558	790	104	566
243	899	000	230				412		349					1232	213		6	131	431	275		226	160	201	3
72%	101 5	C.101	70%		••••		81.2		36%	-				52.1	42.5		%96	73.05	23.93	36%		55.3	303	70.3	83%
	DF01363	Pr01363	emb CAA19842.1				PF00169		gb AAD04568.1					PF00169	PF00169		emb CAB65966.1	7000014	PF00036	pir S14113 S14113		PF00169	0710010	FF00109	sp Q64096 DBS_MO
80H7.5 - fruit fly	(Drosophila melanogaster)	PFAM: FYVE zinc finger	(AL031027)	/prediction=(method:""ge	nefinder"", 111	PROTEIN)"", sp	PFAM: PH domain		(AF102854) membrane-	associated guanylate	kinase-interacting protein.	2 Maguin-2 [Rattus	norvegicus	PFAM: PH domain	DFAM: PH domain	11 AIV. 111 COMM	(AJ250425) Collybistin I	Mattus Hot Vegicus	PFAM: EF hand	1-phosphatidylinositol-	4,5-bisphosphate	PFAM: PH domain	i iid yerda	PrAM: PH domain	GUANINE
	(HMMER 2.1.1	blastx.2				HMMER	2.1.1	blastx.2					HMMER	LINANAED	2.1.1	blastx.2	400	HMMER 1.8	blastx.2		HMMER	2.1.1	HMMEK	blastx.14
		450					21							451	73	67			24			452		453	27
		909949			-		916606							971615	302000	60/066			910073		·	926486		909912	1212624
		HDPSU48					HDPWE80							HDQFY84	OLONOTI	HEONOTA			HFCBB56		·	HFKKZ94		HHBGJ53	HHFJF24

EXCHANGE FACTOR 79% 878 979 DBS (DBLS BIG 23% 512 613 SISTER) (MCF2 1 613 613 SEQUENCE-LIKE PROTEIN 3 107 PROTEIN). PROTEIN 3 107 PRAM: PH (pleckstrin PF00169 23.24 3 107 PFAM: PH (pleckstrin) Sp(63406 DBS_RA 98% 3 158 NUCLEOTIDE T 1 158 613 NUCLEOTIDE T 1 613 613 DBS (DBL'S BIG T 1 42.9 251 487 PEXCHANGE FACTOR gi[397579 emb CAA5 97% 138 263 613 DBS (DBL'S BIG putative [Rattus PF00169 42.9 251 487 PFAM: PH domain PF00169 42.9 352 663 PFAM: PH domain PF00169 42.4 352 663 mitogen inducible gene emb CAA80852.1 61% 1 825	
23% 512 6 PF00169 23.24 3 1 sp Q63406 DBS_RA 98% 3 T	EXCHANGE F
PF00169	DBS (DBLS BIG
PF00169	SISTER) (MCF2
PF00169	TRANSFO
PF00169	SEQUENC PROTEIN)
Sp Q63406 DBS_RA 98% 3 1 1 1 1 1 1 1 1 1	MER
The Factor of the proof of th	1.8 homology)
ACTOR actor <td< td=""><td></td></td<>	
G gil397579 emb CAA5 97% 138 503 2297.1 42.9 503 503 603 604 601 601 601 601 601 601 601 601 601 601	EXCHAI
gi 397579 emb CAA5 97% 138 tain PF00169 42.9 251 emb CAA52297.1 95% 131 ain PF00169 42.4 352 objecte emb CAA80852.1 61% 1 apiens] PF00169 62.3 562 nain PF00169 62.3 562 Imamed gi 7021093 dbj BAA9 98% 97 IHomo 1379.1 57% 589	DBS (DE
gil397579 emb CAA5 97% 138 aain PF00169 42.9 251 emb CAA52297.1 95% 131 ain PF00169 42.4 352 apiens emb CAA80852.1 61% 1 apiens PF00169 62.3 562 nain PF00169 62.3 562 nain PF00169 62.3 562 IFIB-beta dbj BAA75243.1 87% 118 Imamed gi 7021093 dbj BAA9 98% 97 IHomo 1379.1 57% 589	SISTEK) T (FRAGMENT)
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emb CAA52297.1 95% 131 PF00169 42.4 352 ns] PF00169 62.3 562 3-beta dbj BAA75243.1 87% 1118 ned gi 7021093 dbj BAA9 98% 97 nno 1379.1 57% 589	+
gene emb CAA52297.1 95% 131 gene emb CAA80852.1 61% 1 ns] PF00169 62.3 562 3-beta dbj BAA75243.1 87% 118 ned gi 7021093 dbj BAA9 98% 97 nmo 1379.1 57% 589	HMMEK FFAM: FF
gene emb CAA80852.1 61% 1 ns] PF00169 62.3 562 3-beta dbj BAA75243.1 87% 118 ned gi 7021093 dbj BAA9 98% 97 omo 1379.1 57% 589	+
gene emb CAA80852.1 61% 1 ns] PF00169 62.3 562 3-beta dbj BAA75243.1 87% 118 ned gi 7021093 dbj BAA9 98% 97 omo 1379.1 57% 589	-
gene emb CAA80852.1 61% 1 ns] PF00169 62.3 562 3-beta dbj BAA75243.1 87% 118 ned gi 7021093 dbj BAA9 98% 97 nmo 1379.1 57% 589	HMMER PFAM: P 2.1.1
3-beta dbj BAA75243.1 87% 118 ned gi 7021093 dbj BAA9 98% 97 589	
ta dbj BAA75243.1 87% 118 gi 7021093 dbj BAA9 98% 97 1379.1 57% 589	HMMER PFAM:
gi 7021093 dbj BAA9 98% 97 1379.1 57% 589	
1379.1 589	blocty 14 (AKOOO)

424	763	1625	1676	417	849	766	260	352	406	504	3/8	307	100
104	86	1254	3	145	556	173	162	173	188	113	97	C8	104
51.8	72%	60.2	94%	21.29	114.1	43%	37.3	43%	58.6	41%	73	30%	18.44
PF00169	dbj BAA91379.1	PF00169	dbj BAA91711.1	PF00169	PF00169	gi 1688318 gb AAB3 6958.1	PF00169	gi 1688318 gb AAB3 6958.1	PF00169	gb AAC35236.1	PF00169	dbj BAA84651.1	PF00169
PFAM: PH (pleckstrin	(AK000790) unnamed protein product [Homo	sapiens] PFAM: PH domain	(AK001472) unnamed protein product [Homo	PFAM: PH (pleckstrin homology) domain	PFAM: PH domain	SecG [Dictyostelium	PFAM: PH domain	SecG [Dictyostelium	PFAM: PH domain	(AC005496) unknown protein [Arabidopsis thaliana]	PFAM: PH domain	(AB005903) AtPH1 [Arabidopsis thaliana]	PFAM: PH (pleckstrin homology) domain
MER	1.8 blastx.2	HMMER	2.1.1 blastx.2	HMMER 1.8	HMMER 2.1.1	blastx.14	HMMER	blastx.14	HMMER	blastx.2	HMMER 2.1.1	blastx.2	HMMER 1.8
457		458		459	460	35	461	36	462		463	· · · · · ·	464
958656		878592		957912	932133	1188029	909874	1154065	927872		910088		928168
HKABX13		HLTHG77		HLWBZ09	HLWEH54	HLYAA41	HLYAA41	HLYDV62	HLYDV62		HMCFB47		HMSOI20

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90	207	294	358	621	624	437	476	215	482	195	1015	1453		1129	6101	613	955	*	305	504	
343	139	220	293	406		213	414	183	294	10	728	86		20	1097	332	263		363	259	
%98 86%	100%	80%	40%	50.5	26%	36%	42%	72%	30.3	62%	81.4	85%		89%	0//6	81.9	94%		40%	78.3	
gi 1657837 gb AAB1 8198.1			and a grant of the second	PF00169	gb AAB18198.1	oil4756912lemblCAB	42323.1	-	PF00169	emb CAB42187.1	PF00169	2LIA A E 2448 & 11A E 2	10818 1	gi 4835895 gb AAD3	0288.1 AF136450_1	PF00169	gb AAD30288.1 AF1	36450_1	gi 2190355 emb CAA	PF00620	
p116Rip [Mus musculus]				PFAM: PH domain	n 16Rin [Mus musculus]		unnamed protein product		PFAM: PH domain	unnamed protein product	PFAM: PH domain	OF GARRO COROS CONT.	(AF210818) SWAF-70 [Homo saniens]	(AF136450) goodpasture	antigen-binding protein	PFAM: PH domain	(AF136450) goodpasture	antigen-binding protein	racGAP [Dictyostelium	PFAM: RhoGAP domain	
blastx.14				HMMER	\top	Τ,	blastx. 14		HMMER	blastx.2	HMMER	2.1.1	blastx.2	blastx.14		HMMER	2.1.1 blastx.2		blastx.14	HMMER	7.1.1
39	•		4	465			40		466		467			42	!	468			43	469	
1163460				922141			1078178		909928		919836			1164740		910026			1090522	658606	
HOENH55		-		HOENH55			HPIAI01		HPIA101		HPJCT50			HDMEEOI	111 WIL L/1	HPMFE91			HRAED51	HRAED51	

585	528	531	209		966	996	437	532	11111	1136	521	959	8	5		1165		530		11511		177	1/7	487	
259	289		533		811	209	21	425	962	1041	321	57	_			482		252		468		05	99	47	
28%	34.3	7007	76%		34.6	%16	63%	%88	20%	44%	6'88	%68	210%	0/16		87%		54.1		87%		0 %	30.9	77%	
gb AAA40809.1	PF00169		emb CAB63063.1		PF00169	emb CAA52297.1	-	-			PF01363	9b AAC27698.1	201111111111111111111111111111111111111			gil7019925 dbj BAA9	0927.1	PF00169		dbj BAA90927.1			PF00169	dbj BAA92229.1	
beta-chimaerin [Rattus	PFAM: PH domain		(AL096767) dJ579N16.2 (SET hinding factor 1)	(Homo sapiens]	PFAM: PH domain	mitative [Rattus	norvegicus	[222.52.101]		,	PFAM: FYVE zinc finger	(AE038388) actin-	(Al 00000 bound	filament binding protein	Frabin [Rattus norvegicus]	(AK000074) unnamed	protein product [Homo	PFAM: PH domain		(AK000074) unnamed	protein product [Homo	Sapiens	PFAM: PH domain	(AK000004) FLJ00004	protein [Homo sapiens]
blastx.2	HMMER	2.1.1	blastx.2		HMMER 2 1 1	blacty 7	Z:vicaio .				HMMER 2.1.1	bloctv 7	Ulasta.2			blastx.14		HMMER	2.1.1	blastx.2			HMMER 2 1 1	blastx.2	
	470				45						46					47		471	:				472	 	
_	924885			,	914775					-	909749	•				1090524	,	010027	770017				909752		
	HSMBA19				HSYCY88						HTEDW26					HTEKD92		UTTER D02	HIEND92	1			HTLDT05		

440	458 58	348	601	1787	762	1002	1131	837	1671	653	.341	341	929	1207	069	1034	359	677	1021	716	710
132	75	19	1423	1192	700	688	1054	808	1552	009	57	9	7111	1139	550	957	69	3	1653	516	78
65.3	79%	62%	/0%	42%	47%	23%	42%	%08	27%	38%	38.8	53%	31%	65%	32%	42%	63.5	45%	20%	6.68	20%
PF00169	emb CAA52297.1	sp BAA91043 BAA9	1043					2			PF00169	dbilBAA91043.11	-				PF00169	dbj BAA24267.1	gi 3292902 emb CAA 19842.1	PF01363	emb CAA19842.1
PFAM: PH domain	putative [Rattus	CDNA FLJ20260 FIS,	CLONE COLF7627.							•	PFAM: PH (pleckstrin	(AK000267) unnamed	protein product [Homo	saniens]			PFAM: PH domain	(AB008430) CDEP [Homo sapiens]		PROTEIN)"", sp PFAM: FYVE zinc finger	(AL031027)
HMMER 2.1.1	blastx.2	blastx.14								-	HMMER	hlastx 2					HMMER 2.1.1	blastx.2	blastx.14	HMMER	2.1.1 blastx.2
473		50									474						475	-	52	476	
529764		1194698		,							878606						944393		1150195	909919	•
HTPDS90		HTPHM71									HTPHM71						HUUAR12		HWAGP22	HWAGP22	

906968 53 HMMER 1.8 blastx.2 blastx.14 b10018 477 HMMER 2.1.1 blastx.2 blastx.2	PROTEIN)"", sp PFAM: PH (pleckstrin homology) domain brain beta spectrin [Mus musculus] CG1513 PROTEIN.	PF00169			
53		PF00169			000
54 477	 		60.73	39	333
54	 	gb AAC42040.1	30%	93	386
477		sp Q9V5D4 Q9V5D4	64%	1445	1924
477			%99.	2	355
477			33%	1943	2218
477	-		52%	518	280
477	,		24%	1295	1393
477			38%	68	147
blastx.2	PFAM: PH domain	PF00169	43	∞	241
	(AF000195) Contains	gb AAC24270.1	63%	14	241
-			33%	238	414
	domain: PF00169 (PH), 1				
909833 478 HMMER		PF00433	57.51	287	445
1.8	-		/0001	750	140
blastx.2	(AJ245709) Akt-3 protein [Homo sapiens]	emb CAB53537.1	100%	230	116
937850 56 HMMER	1-	PF00069	212.5	89	598
2.1.1			, 600	0,	000
blastx.2	(AF169035) protein	gb AAF12758.1 AF1 69035		 89	678
1153870 57 hlastx 14	+-	gi 5006445 gb AAD3	%66	9	191
·		7506.1 AF128625_1			
	beta [Homo sapiens]				t
661045 480 HMMER	R PFAM: Protein kinase C	PF00433	21.1	679	(9/

Mask Mask				211	terminal domain				
1152249 59 101 55 50 50 50 50 50 5				Flooty 7	(AE128625) CDC42-	gb AAD37506.1 AF1	%16	289	1179
1152249 59 148 158 150 1				Uldsta.2	Linding protein kingse	28625 1	%66	101	595
1152249 128625 124000 sapiens 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 180006445 gb AAD3 1800069				-	Uniting protein winds		23%	862	1152
974253 481 blastx.14 (AF128625) CDC42- gil5006445 gb AAD3 99% 22% 904 111 974253 481 blastx.14 (AF128625) CDC42- gil5006445 gb AAD3 99% 357 802 804 111 14 974255 58 HMMHER PFAM: Eukaryotic protein Rinase domain beta Homo sapiens 1152249 59 blastx.14 (AF128625) CDC42- gb AAD37506.1 AF1 98% 72 804 157 111 1152249 59 blastx.14 (AC004877) sc-spondin- gil3638957 gb AAC3 34% 824 824 824 824 824 824 824 824 824 824					peta [Homo sapiens]		18%	922	1140
974253 481 blastx.14 (AF128625) CDC42- gij5006443[gb]AAD3 99% 2 22% 904 111 bhat Blastx.14 (AF128625) CDC42- gij5006443[gb]AAD3 99% 357 357 357 357 357 357 357 357 357 357							25%	937	1152
974253 481 blastx.14 (AF128625) CDC42- gij5006445[gb]AAD3 99% 2 2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5			÷				22%	934	1170
974253 481 blastx.14 (AFI28625) CDC42- gij5006445jgbjAAD3 99% 2 357 55 14 974253 481 blastx.14 (AFI28625) CDC42- 1506.1 AF128625_1 66% 357 55 50 357 50 357 50 350 50 350 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>22%</td> <td>904</td> <td>1161</td>							22%	904	1161
9/4255 481 Outstart Outst		0.70	401	Llooty 14	(AE128625) CDC42-	ei 5006445 eb AAD3	%66	2	328
4 974255 58 HMMER PFAM: Eukaryotic protein PF00069 244.21 22% 32.5 32.5 32.6 32.8 32.5 32.8 32.8 32.8 32.8 32.8 32.8 32.8 32.8	HE6BK63	974255	184	DIASIX.14	(AI 128023) CCO IZ	7506.11AF128625 1	%99	357	200
4 974255 58 HMMER PFAM: Eukaryotic protein PF00069 244.21 25% 53% 523 53% 53% 523 53% 53% 523 53% 53% 523 53% 53% 53% 53% 53% 53% 53% 53% 53% 53		2			bote [Homo caniene]	1	100%	502	570
4 974255 58 HMMER PFAM: Eukaryotic protein Pf00069 244.21 297 10 blastx.2 (AF128625) CDC42- gb AAD37506.1 AF1 22% 1572 10 blastx.14 (AC00487) sco-spondin- gi 3638957 gb AAC3 68% 137 mucin-ilke; similar to p98167 1 sapiens] 2 909835 482 HMMER PFAM: Protein kinase C pF00433 33.87 943 11 blastx.2 human protein kinase B emb CAA43372.1 89% 943 11 blastx.14 (AF097887) Cbp Pfattus gi 3806122gb AAC6 100% 75 blastx.14 (AF097887) Cbp Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfattus gi Pfa					Deta [1101110 sapietis]		22%	137	325
4 974255 58 HMMER PFAM: Eukaryotic protein Pf00069 244.21 297 10 4 974255 58 HMMER PFAM: Eukaryotic protein Pf00069 244.21 297 10 53% 523 523 523 523 523 523 523 523 523 523							100%	330	362
4 974255 58 HMMER PFAM: Eukaryotic protein PF00069 244.21 297 10 1.8 kinase domain blastx.2 (AF128625) CDC42- gblAAD37506.1 AF1 22% 1572 11 blastx.2 (AF128625) CDC42- gblAAD37506.1 AF1 22% 1572 11 beta [Homo sapiens] 28625_1 22% 1572 11 mucin-like; similar to 6301.1 42% 227 34% 227 34% 34% 3332 34% 34% 3332 34% 3387 34% 3332 34% 34% 3332 34% 3387 34% 332 34% 34% 332 34% 332 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 332 34% 34% 34% 34% 34% 34% 34% 34% 34% 34%					,		55%	325	378
4 974255 58 HMMER PFAM: Eukaryotic protein PF00069 244.21 297 10 1.8 kinase domain 1.8 kinase domain 1.8 beta [Homo sapiens] 1152249 59 blastx.14 (AC00477) sco-spondin-gil3638957[gb]AAC3 68% 137 mucin-like; similar to mucin-like; similar to p98867 1 sapiens] 2 909835 482 HMMER PFAM: Protein kinase C pF00433 33.87 943 118 blastx.2 human protein kinase B emb CAA43372.1 899% 943 11 [Homo sapiens] 8 1001088 60 blastx.14 (AF097887) Chp [Rattus gil3806122[gb]AAC6 1100% 75							32%	242	325
4 974255 58 HMMER PFAM: Eukaryotic protein kinase domain PF00069 244.21 297 10 1.8 kinase domain glastx.2 (AF128625) CDC42- gblAAD37506.1 AF1 98% 72 17 18<					-		53%	523	561
1.8 kinase domain 1.8 kinase domain 1.8 kinase domain 1.8 kinase domain 1.8 kinase domain 28625_1 22% 1572 1 152249 59 blastx.14 (AC004877) sco-spondin-gij3638957 gb AAC3 68% 137 227 1 152249 59 blastx.14 (AC004877) sco-spondin-gij3638957 gb AAC3 68% 137 227 1 152249 59 blastx.14 (AC004877) sco-spondin-gij3638957 gb AAC3 24% 258	HFKDR14	974255	58	HMMER	PFAM: Eukaryotic protein	PF00069	244.21	297	1097
blastx.2 (AF128625) CDC42- gb AAD37506.1 AF1 98% 72 1 152249 59 blastx.14 (AC004877) sco-spondin- gi 3638957 gb AAC3 68% 137 1 1152249 59 blastx.14 (AC004877) sco-spondin- gi 3638957 gb AAC3 68% 137 1 1 1 1				1.8	kinase domain				1222
beta [Homo sapiens] 1152249 59 blastx.14 (AC004877) sco-spondin-gi]5638957[gb]AAC3 68% 137 mucin-like; similar to 6301.1 42% 569 P98167 1 sapiens] 2 909835 482 HMMER PFAM: Protein kinase C PF00433 1.8 terminal domain blastx.2 human protein kinase B emb CAA43372.1 89% 943 1		-		blastx.2	(AF128625) CDC42-	gb AAD37506.1 AF1	%86 %86	1572	1706
1152249 59 blastx.14 (AC004877) sco-spondin-gil3638957 gb AAC3 68% 137 mucin-like; similar to 6301.1 42% 569 p98167 1 sapiens 50% 337 p98167 1 sapiens 50% 34% 332 p98167 1 sapiens 54% 84 reminal domain 61% 61% 61% 61% 61% 61% pastx.2 human protein kinase B emb CAA43372.1 89% 943 1 pastx.14 (AF097887) Chp [Rattus gil3806122 gb AAC6 100% 75					binding protein kinase	28625_1	77%	7/61	00/1
1152249 59 blastx.14 (AC004877) sco-spondin-gi[3638957 gb AAC3 68% 157 157					beta [Homo sapiens]				00
mucin-like; similar to 0301.1 42% 569 569 387 34% 332 34% 34% 84 84 84 84 84 84 84	HFPER82	1152249	59		(AC004877) sco-spondin-	gi 3638957 gb AAC3		137	90
909835 482 HMMER PFAM: Protein kinase C PF00433 33.87 943 1 1.8 terminal domain blastx.2 human protein kinase B emb CAA43372.1 89% 943 1 [Homo sapiens] 609 hlastx.14 (AF097887) Chp [Rattus gi]3806122[gb]AAC6 100% 75					mucin-like; similar to	0201.1	7000	695	513
909835 482 HMMER PFAM: Protein kinase C PF00433 33.87 943 1 1.8 terminal domain blastx.2 human protein kinase B emb CAA43372.1 89% 943 1 1.091088 60 blastx.14 (AF097887) Chp [Rattus gi]3806122[gb]AAC6 100% 75					P98167 1 sapiens]		2005	387	346
909835 482 HMMER PFAM: Protein kinase C PF00433 33.87 943 1 1.8						-	340%	332	255
909835 482 HMMER PFAM: Protein kinase C PF00433 33.87 943 1 1.8 terminal domain emb[CAA43372.1] 89% 943 1 blastx.2 human protein kinase B emb[CAA43372.1] 89% 943 1 [Homo sapiens] [Homo sapiens] 75 75							54%	48	52
909835 482 Highlight Transmand domain 1.8 terminal domain blastx.2 human protein kinase B emb CAA43372.1 89% 943 1 [Homo sapiens]			0.07	TRANCED	DEAM. Protein kingse	PF00433	33.87	943	1047
blastx.2 human protein kinase B emb CAA43372.1 89% 943 1	HFPER82	68835	487	HIMIMIER 18	r Frant. Forcin kings C				
[Homo sapiens] [Homo sapiens] 75 100% 75 1001088 60 blastx, 14 (AF097887) Chp [Rattus gil3806122 gb AAC6 100% 75				blastx.2	human protein kinase B	emb CAA43372.1	%68	943	1053
1001088 60 blastx.14 (AF097887) Chp (Rattus gi]3806122[gb]AAC6 100% /2					[Homo sapiens]			31	090
	HAAAO58	1091088	09	blastx.14	(AF097887) Chp [Rattus	gij3806122 gb AAC6	100%	C/	707

				norwegicus	9198.11			
				i. J. Graffavion	0500071	0.58	75	365
HAAAO58	912622	483	HMMEK	PFAM: Kas tamily	FF00071)		
			2.1.1 hlaetx 2	(AF097887) Cho [Rattus	gb AAC69198.1	%86	75	467
			1:000	norvegicus)				
HADFK69	1091937	19	blastx.14	(AF229839) kappa B-ras	gi 7008402 gb AAF34	%16	207	752
٠			,	1 [Homo sapiens]	1.866			573
HADFK69	912850	484	HMMER	PFAM: Ras family	PF00071	85.8	109	5/5
			1.8	(contains ATP/GTP				
				binding P-loop)				
			blastx.2	(AF229839) kappa B-ras	gb AAF34998.1	 %06	49	543
				l [Homo sapiens]			000	703
CHOMMOR	1152329	62	blastx.14	rab-related GTP-binding.	gi 1491714 emb CAA	38%	303	990
700W 1711] }		nrotein [Homo sapiens]	68227.1	. 64%	145	303
					-	20%	31	96
C9OMdUH	912722	485	HMMER	PFAM: Ras family	PF00071	132.39	127	432
			1.8	(contains ATP/GTP				
				binding P-loop)				
			blastx.2	rab-related GTP-binding	emb CAA68227.1	54%	133	444
				protein [Homo sapiens]		57%	07	0/
HDPMO85	912837	486	HMMER	PFAM: Ras family	PF00071	75.28	162	899
			1.8	contains ATP/GTP				
				binding P-loop)			1	i
		<u>,</u>	blastx.2	(AF229840) kappa B-ras	gb AAF34999.1	95%	147	61/
				2 [Homo sapiens]				too
HDPUY72	966153	487	HMMER	PFAM: Ras family	PF00071	325.7	818	707
			2.1.1			/0001	150	210
			blastx.2	(AF112206) ras-related	gb AAF17194.1 AF1	100%	100	717
				protein rab-14 [Homo	12206_1	•		
				sapiens		/0//0	00	120
HDTF87	1154640	65	blastx.14	GTP-binding protein	gi 409166 gb AAA34	%96	188	+67

				[Volvox carteri]	253.1			
TINTIE07	70220	488	HMMER	PFAM: Ras family	PF00071	198.2	110	394
HUIJF0/	176106	900	2.1.1					
	·		blastx.2	strong similarity to the	gb AAB52431.1	%26	68	394
				YPT1 sub-family of RAS		73%	396	/3/
				proteins [Caenorhabditis				
			3	elegans			T C	1075
HE8TB94	1178794	99	blastx.14	ras-like protein [Homo	gi 190881 gb AAA36	78%	507	548
				Sapiciis	11.11.	7363	605	1104
HE8TB94	935935	489	HMMER	PFAM: Ras family	PF00071	730.3	(7)	
			blastx.2	ras-like protein [Homo	gb AAA36547.1	%08	523	1101
				sapiens			t	767
HE8UB55	912932	490	HMMER	PFAM: Ras family	PF00071	271.56	1.61	9/9
			×.	(contains A1F/O1F)				
	. <u>. </u>		blastx.2	(AL049685) hypothetical	emb CAB41256.1	%68	185	889
				protein [Homo sapiens]				0,0
HEBGA65	1178633	89	blastx.14	Rab24 protein [Mus	gi 438164 emb CAA8	%06 %V0	435	098
				musculus	04 / 2.1	0/4/	0/01	000
HEBGA65	912815	491	HMMER	PFAM: Ras family	PF00071	176.38	451	939
			1.8	(contains ATP/GTP				
				binding P-100p)		200	CVV	1035
			blastx.2	Rab24 protein [Mus	emb CAA80472.1	9776	744	CCOI
				musculus		, out •	100	000
HEGRR\$9	1197907	69	blastx.14	RAS-LIKE PROTEIN	sp P03967 RASD_DI	4/%	1/0	976
(IFCER)) 		RASD	CDI	57%	497	6/9
				(TRANSFORMING		53%	944	988
			•	PROTEIN P23).				,
HEGBB59	912601	492	HMMER 1 8	PFAM: Ras family (contains ATP/GTP	PF00071	75.96	370	546
	_	_	1.0	(Communa transfer				

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2000	53%	156.24		%90	0/0/		030%	73.70	305.73			72%	7000	%/6	95%	,142.21	_		97%	93%	254.6		/000	99%6	/0001	100%	
	emb CAA77070.1	PF00071		114 4 13 4 3 0 3 4 11	go[AAD45054.1]		D34 41001100114 41	sp AAr6/102 AAr0/ 162	PF00071			dbj BAA84707.1		gi 4587775 gb AAD2	5874.1	PF00071			gb AAD25874.1		PF00071		7	emb CAA80473.1		gi 6002585 gb AAF00 048.1 AF091035_1	
	ras protein [Suberites	family	(contains ATP/GTP	1	pa Ba	GTP-binding protein	Homo sapiens	GTPase Rab37.		(contains ATP/GTP	binding P-loop)	(AB027137) RAB-26	[Homo sapiens]	(AF058807) GTP-binding	protein rah [Bos taurus]	PFAM: Ras family	(contains ATP/GTP	binding P-loop)	(AF058807) GTP-binding	protein rah [Bos taurus]	PFAM: Ras family	(contains ATP/GTP	binding P-loop)	Rab22a protein [Canis	[familiaris]	(AF091035) GTP-binding protein RAB21 [Homo	sapiens]
	blastx.2	+	1.8		blastx.2			blastx.14	HMMER	1.8		blastx.2		blastx.14		HMMFR	8	2	blastx.2		HMMER	1.8		blastx.2		blastx.14	
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		956003					,	1212646	907532	1				1152242	110011	1111000	1117/6				964258					1092116	
	,	HEI HC48						НЕООН90	UEOOHOO	TIECQUIVO				HEVLIA 19		TIEVITATO	HFNTAIO				HFKMA10	O I WINTER HI				HHBFM91	

340	316		416	419	594	452	593	717	10	. 685	613	338	407	407
2	2		3	3	229	297.	228		90	113	53	102	3	3
86.13	97%		211.1	100%	81%	103.6	81%	7000	0/86	231.3	%66	100%	150.75	97%
PF00071	gb AAF00048.1 AF0	91035_1	PF00071	dbj BAA84707.1	gi 3859936 gb AAC7	PF00071	gb AAC72918.1		gi 7020212 dbj BAA9 1034.1	PF00071	dbj BAA91034.1	gi 5107835 gb AAC5 1194.2	PF00071	gb AAC51194.2
PFAM: Ras family (contains ATP/GTP	binding P-loop) (AF091035) GTP-binding	protein RAB21 [Homo sapiens]	PFAM: Ras family	(AB027137) RAB-26	(AF081353) GTP-binding	PFAM: Ras family	(AF081353) GTP-binding	protein [Homo sapiens]	(AK000254) unnamed protein product [Homo	PFAM: Ras family	(AK000254) unnamed protein product [Homo	sapicits] small GTP-binding protein Rab27b [Homo	Sapiens) PFAM: Ras family (contains ATP/GTP	binding P-100p) small GTP-binding
HMMER 1.8	blastx.2		HMMER	blastx.2	blastx.14	HMMER	2.1.1 blastx.2		blastx.14	HMMER	blastx.2	blastx.14	HMMER 1.8	blastx.2
495		-	75		9/	496			11	497		78	498	
912832			912715		1134410	912580			1154790	912628	-	1078090	912836	
HHBFM91			HIBBF63	,	HMCEI38	HMCEI38			НММЈД68	HMWJD68		HOEOL58	HOEOL58	

	54 677	999 55	43 666	192 872		162 872	707	774 007			216 281		39 /4	201 521				248 268		306 740	-1.	717		993 1433
	100%	310.6	%001	242.77		1 %66		73.55			63% 2			30%				85%		205.32	•			94.19
.,			1)[247			ľ										•			7(
	gi 919 emb CAA3980	PF00071	emblCAA39800.11	PF00071		dbj BAA87324.1		PF00071		gb AAA31261.1			gi 286238 dbj BAA02	500.1						PF00071			emb CAB41256.1 	PF00071
protein Rab27b [Homo	saptens] rab4b [Canis familiaris]	PFAM: Ras family		PFAM: Ras family	(contains ATP/GTP	(AB034244) RAB23	protein [Homo sapiens]	PFAM: Ras family	(contains ATP/GTP	small GTP-binding	protein [Oryctolagus	cuniculus	N-methyl-D-aspartate	receptor subunit [Rattus	rattus	1				PFAM: Ras family	(contains ATP/GTP	binding P-loop)	(AL049685) hypothetical	PFAM: Ras family
	blastx.14	HMMER	2.1.1	HMMER	1.8	blastx.2		HMMER	1.8	blactx 2			blastx.14)	HMMER	1.8		blastx.2	HMMER
	62	499		500)))			81					82							201	· ·			502
	1162856	912776		912812	71071/			971281					997659							912947				859890
	HRACA51	HRACA51		CENVHON	2C V ALICIT			HTPDE66					HTPDV73							HTPDV73				TEDITESS

	1478	1014	921	CL9	2/0	100	900	2 2	667		308	000		278		275			069		321	C/#		101	095	(0)	
	993	793	664	100	490	166	c,	74	m m		177	±,		18		54			85		117	011		70	00	//#	
	83%	93%	170%	4//0	57%	53%	000	80.7	43%	 	/000	0%88	•	171	101	100%			%96			147.95		è	98%	-0%08 -0%08	
	gb AAD51377.1 AF0	95350_1	Id do a dimogram	sp P03967 KASD_D1	CDI			PF00071	emb CAA78508.1			pir S30096 S30096			PF000/1	abl A C 69218 11	li:017/000vlng		gi 206543 gb AAA42	000.1		PF00071			gb AAA42000.1		
(contains ATP/GTP	Omding 1-100p)	protein 2A [Homo	sapiens	RAS-LIKE PROTEIN	RASD	(TRANSFORMING	PROTEIN P23).	PFAM: Ras family	ras-related protein	[Dictyostelium	discoideum]	GTP-binding protein ypt1	[similarity] - Neurospora	crassa	PFAM: Ras family	(AE101210) similar to	(AF101510) Similar to	KAS-felated proteins,	rab-related GTP-binding	protein [Rattus	norvegicus]	PFAM: Ras family	(contains ATP/GTP	binding P-loop)	rab-related GTP-binding	protein [Rattus	norvegicus
1.8	Llooty 2	Diastx.2		blastx.14				HMMER	blastx.2			blastx.14			HMMER	2.1.1	blastx.2		blastx.14			HMMER	1.8		blastx.2		
				84				503				85			504				98)		505					
				1224609				912929				1225329			912672				1182321			931547					
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747	1011	717	720	764			716	562	562	000	889	688	210	010	373	467	483	160	335	455	156
391	742	394	391	726			81	86	71		311	287	100	194	2	381	460	131	270	165	103
9776	94%	143.42	95%	%9 <i>L</i>			95%	301.8	%06		298.2	100%	5	13	85%	%6L	87%	20%	22.95	43%	38%
sp Q9XS71 Q9XS71		PF0007.1	gb AAB20669.1			4	gi 206537 gb AAA41 995.1	PF00071	gb AAA41995.1		PF00071	dbj BAA89542.1		PF00018	dbj BAA19686.1				PF00018	gb AAA96115.1	
GTP-BINDING	PROTEIN RAH (FRAGMENT).	PFAM: Ras family (contains ATP/GTP	LMW G-protein=low-	molecular-weight GTP-	binding protein [mice,	HT4 neural cell line, Peptide, 208 aal [Mus sp.]	RAB15 [Rattus	PFAM: Ras family	RAB15 [Rattus	norvegicus	PFAM: Ras family	(AB036693) RAB9-like	protein [Homo sapiens]	PFAM: Src homology domain 3	Kryn [Mus musculus]				PFAM: Src homology	coded for by C. elegans	cDNA yk34a9.5; coded
blastx 14		HMMER 1.8	blastx.2				blastx.14	HMMER	blastx.2		HMMER	blastx.2		HMMER	hlastx 2				HMMER 1.8	blastx 2	
87	à	909					88	507			508			06			-		509		
1228064	1008771	972413					1178825	912581			912842			963811					895963		
HWAHD40	TWAIID49	HWAHD49					HWLGG31	HWLGG31			HWLKF25			Н2СВН45					HAGDN53		

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	1306	4017	785	791		510	684	.376	397	308	79	887 979 500
·	1136	4511	615		729	445	99.	212	14	392	33	45 702 887 381
	67.14	29%	68.5	93%	93%	4.07	95%	49.7	41%	53.06	4.22	96% 74% 100% 52%
	PF00018	dbj BAA91729.1	PF00018	gb AAF04472.1 AF1 30979_1	gi 1778500 gb AAB4 0783.1	PF00018	gb AAB40783.1	PF00018	emb CAA55394.1	PF00018	PF00018	gi 4104812 gb AAD1 1957.1
for by C. elegans 1	PFAM: Src homology	(AK001509) unnamed protein product [Homo	sapiens] PFAM: SH3 domain	(AF130979) SH3 domain- containing protein 6511	ferrienterobactin receptor. precursor [Escherichia	PFAM: Src homology	ferrienterobactin receptor precursor [Escherichia	PFAM: SH3 domain	p115 [Homo sapiens]	PFAM: Src homology domain 3	PFAM: Src homology domain 3	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo
	HMMER	tx.2	HMMER	blastx.2	blastx.14	HMMER	blastx.2	HMMER	2.1.1 blastx 2	HMMER 18	HMMER 1.8	blastx.14
	92		93		94	510		95		96	16	86
	971347		908173		1150790	878322	-	909782		945088	522739	1175204
	HAMFM39		HBGQT03		HBGSJ13	HBGS113	,	HBIBQ89		НСЕСМ90	НСЕРН71	HCFMT57

461	386	319	803	830	243	1770	518	243	830	684	153	699	137	717	717	231	188	230	227	3	n				722	371	100	161
381	327	161	744	780	160	1693	468	190	795 .	622	73	209	54	643	631	136	111	114	144	107	377		24 ·		456	189	67/) 54 126
44%	55%	28%	20%	58%	35%	34%	47%	55%	28%	42%	29%	42%	35%	36%	31%	25%	38%	28%	28%	14.55	%96				44%	965	46%	23%
											-					-				PF00018	gb AAD11957.1				gi 530823 gb AAA62	280.1		
	sapiens	-,	-					`					-							PFAM: Src homology	(AF039571) peripheral	benzodiazepine receptor	interacting protein; PBR-	IP/PKAX1 [Homo	enidermal growth factor	receptor kinase substrate	[Homo sapiens]	•
		_		•			- <u>-</u>		,											HMMER	blastx.2		*		blastx 14			
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					BE00016	50.48	178	342
HCOMM05	925952	512	HMMER 1.8	PFAM: Src homology	Frounts	01.00		
			blastx 2	epidermal growth factor	gb AAA62280.1	46%	445	840
				receptor kinase substrate		43%	115	455
				[Homo sapiens]		23%	43	777
HC00Z11	965306	100	HMMER	PFAM: Src homology	PF00018	5.22	179	214
			1.8	domain 3		10001	100	085
			blastx.2	(AL022238) dJ1042K10.2	emb CAA18266.1	100%	781	700
				(supported by				
				GENSCAN, FGENES and	-		-	
				GENEWISE) [Homo		_		
				sapiens			077	101
HCWFF88	506577	101	HMMER	PFAM: Src homology	PF00018	4.92	140	101
			1.8	domain 3			170	413
HDMAV01	911386	513	HMMER	PFAM: Src homology	PF00018	57.13	+07	- C1+
			1.8	domain 3			-	017
			blastx.2	unnamed protein product	emb CAB42388.1	73%	7	116
				[unidentified]		100%	C	010
HDPDA47	929193	103	HMMER	PFAM: Src homology	PF00018	12.52	691	018
			1.8	domain 3				7001
			blastx.2	(AL049683) hypothetical	emb CAB41255.1	%69	145	9701
		٠		protein [Homo sapiens]		53%	945	2701
HDPFF24	909232	104	HMMER	PFAM: KRAB box	PF01352	121.3	158	349
			2.1.1		00 111 707000	/00/2	158	457
	·		blastx.2	(AC007228) R31665_2	gb AAD23606.1 AC0	30%	100	Ĉ.
				[AA 1- 673] [Homo saniens	0/228_1			
HDPP035	966248	105	HMMER	+-	PF00018	14.07	009	749
			1.8	-+		300%	. 78	1148
			blastx.2	(AL049683) hypothetical	emb[CAB41255.1]	39%	1,0	1110

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				protein [Homo sapiens]				
HDPSR74	911396	901	HMMER	PFAM: Src homology	PF00018	47.19	293	460
			1.8	domain 3		200	100	633
			blastx.2	(AF104246) enhancer of	gb AAD11795.1	48%	187	CCC
				filamentation 1 homolog	-			
				[Gallus gallus]		1000	027	3175
HDTKQ14	886936	107	HMMER	PFAM: Src homology	PF00018	17.71	430	0
			1.8	domain 3		/0001	130	555
			blastx.2	(AL049683) hypothetical	emb[CAB41255.1]	0,001	75	200
				protein [Homo sapiens]		26%	0/	167
COGO	1150007	100	blacty 14	(A 1007012) Fish protein	gi 3702174 emb CAA	75%	795	613
HEOGF02	1130897	001	Olasta: 17	(Mus musculus)	07416.11	%99	603	427
		-		[winstillasinas		10%	681	02
						39%	603	430
						40%	804	613
					-	38%	792	637
						39%	795	637
						41%	009	427
						38%	582	433
						37%	552	481
					-	37%	150	70
						20%	532	485
				,		54%	459	427
HE6GF02	911263	514	HMMER	PFAM: Src homology	PF00018	51.15	10	174
.,			8.1	(A 1007012) Eich protein	emblC A A 07416 11	77%	10	186
			blastx.2	(AJUU/ULZ) FISH protein		44%	201	275
HE8PK12	909884	109	HMMER	PFAM: Src homology	PF00018	58.12	161	361
	-		1.8	domain 3				676
			blastx.2	(AF136380) SH3P12	gb AAD27647.1 AF1 36380 1	82%	96	307
67400411	1011176	110	HMMFR	PFAM: Sre homology	PF00018	47.65	268	435
HE9SE02	1 91 14 70	211	Invitation	77				

			1.8	domain 3				
			blastx.2	07) FLJ00007	dbj BAA92232.1	43%	4 677	435
		,		protein [Homo sapiens]		10 01	216	183
HEOPL36	968826	515	HMMER 1.8	PFAM: Src homology	PF00018	19.81	310	407
			Llooty 7	58) d1437M21 3	emblCAB51395.11	%66	178	486
			Diasta.2					
				casein kinase substrate in		-		
				neurons 2) [Homo			• • • • • • • • • • • • • • • • • • • •	
				sapiens]			100	0,0
HFBDJ13	911264	112	HMMER	PFAM: SH3 domain	PF00018	78.6	601	697
			2.1.1			/001	6	173
			blastx.2	(AF030131) Plenty of	gb AAC40070.1	0/8/	C	
				SH3s; POSH [Mus				
	_			musculus]			0,	000
HFTDF15	657020	113	HMMER	PFAM: Src homology	PF00018	4.85	168	507
-			1.8	domain 3				000
ННЕQV39	932851	114	HMMER	PFAM: Src homology	PF00018	30.41	976	90/
			1.8	domain 3			3000	5591
HHFCK09	965304	115	HMMER	PFAM: TBC domain	PF00566	1.9.1	5067	6601
•			2.1.1			è	3000	0701
			blastx.2	(AL022238) dJ1042K10.2	emb CAA18266.1	%/6	7207	380
-				(supported by		98%	0/71	787
				GENSCAN, FGENES and				
				GENEWISE) [Homo			-	
				sapiens				
HISDS62	935932	116	HMMER	PFAM: RhoGEF domain	PF00621	51.3	229	486
			2.1.1	(A 1050405) Collubiatin I	emblCAB65966 11	%96	_	483
 			blastx.2	[Rattus norvegicus]			!	
UI ODT35	839777	117	HMMER	PFAM: Src homology	PF00018	3.85	342	419
לכות אחנו	1111100							

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510	CIC	1554	449		132	27	429			558		846 3 193	9 238		0/7	2 429	
737	161	4	21	58	37	350	241		2.26	322		196	209		199	382	
	149	85%	%88	28.13	93%	%16	169.7		91%	35.3		%16 %86	4 97		4.76	4.09	
	PF00018	gb AAD34595.1 AF1 46277_1	gi 4960047 gb AAD3 4595.1 AF146277_1	PF00018	gb AAD19748.1	gi 5080758 gb AAD3	9268.1 AC007842.5 PF01352		gb AAD39268.1 AC0	PF00595		gb AAD45919.2 AF1 62130_1	p. 000016	Pronota	PF00018	PE00018	
saniens	PFAM: SH3 domain	(AF146277) adapter protein CMS [Homo	sapiens] (AF146277) adapter protein CMS [Homo	sapiens] PFAM: Src homology	domain 3 (AF132480) Ese2 protein	[Mus musculus] (AC007842) BC331191_1	[Homo sapiens]	FFAM. MICED 50%	(AC007842) BC331191_1	[Homo sapiens]	(Also known as DHR or	GLGF). (AF162130) MAGUK protein TEM-61 [Homo	sapiens	PFAM: Src homology	PFAM: Src homology	domain 3	PFAM: Src nomousy
	AER	2.1.1 blastx.2	blastx.14	HMMER	1.8 blastx.2	blastx.14	ady of an	HMIMEK	blastx.2	900	HMMEK 2.1.1	blastx.2		HMMER	I.8 HMMER	1.8	HMMEK
	124		516	517		126		518			127			128	129		130
_	946988		972348	935465		1150018	1120210	885806			911293			695656	773025		917180
_	HNSAA28		HNSAA28	HOGEO43		OHUMIUM	НООДНІЯ	HOUDH19			HOUFT36			HPMFL08	LID CM/D40) AMONIII	69IIQSH

647	863 848 848	218	. 331	169	1991		238		701	1340	0.00	CC5.1	186	901	061	289	739		701
483	3 , 6 , 222	195	366	77	39	3	312		91	1152		3	160	Ć	4	8	647		
249.3	98% 30% 33%	5.33	4.36	36.33	/900	0//6	4 51		37.78	9.14		94%	4.14		15.82	51%	20.78	07:07	67%
PF00018	emb CAB61374.1	PF00018	PF00018	PF00018		gb AAD34595.1 AF1 46277_1	0100000	PF00018	PF00018	0100010	Propose	emb CAB61362.1	0100000	Fruuls	PF00018	emb CAB41255.1		PF00018	emb CAA71414.2
PFAM: SH3 domain	(AL133047) hypothetical protein [Homo sapiens]	PFAM: Src homology	domain 3 PFAM: Src homology	domain 3	domain 3	(AF146277) adapter protein CMS [Homo	sapiens	PFAM: Src homology	domain 3 PFAM: Src homology	domain 3	PFAM: Src homology	(AL133030) hypothetical	protein [Homo sapiens]	PFAM: Src homology	PFAM: Src homology	domain 3 (AI,049683) hypothetical	protein [Homo sapiens]	PFAM: Src homology	domain 3 Graf protein [Homo
AER	2.1.1 blastx.2	HMMER			TIMINICIA 1 8			HMMER	1.8 HMMER	1.8	HMMER	1.8 blactx 2	Diagra:	HMMER	HMMER	1.8 blactv 2	Diasta:	HMMER	1.8 blastx.2
131		519		133	075			135	136		137		-	138	139			140	
949151		573345	00000	600/00	6896/4			954614	751085	C06167	922923			503313	911390			933357	
HSDSB06				HSSAX53	HSVAW49			HTEAG49	E)IIG Auto	HILBH0/	HTLJC71			HTPAD46	LITTV DA7	NI INI NI		HUCOW17	

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726102 141 HMMER 1.8 blastx.2 690442 521 HMMER blastx.2 1151387 143 blastx.14 909682 522 HMMER 1.8	PFAM: Src homology		83%	756	508
141 521 7 143				-	
141 521 7 143	+-		40%	187	246
521		PF00018	5.01	325	387
521	domain 3	abi A B33461 11	74%	3	203
521	Ubs=Ubi guanine		72%	319	417
521	nucleotide exchange factor homolog [mice,		73%	203	259
521	32D 1	-			255
143	PFAM: Src homology	PF00018	31.65	71	255
143	(AF178432) SH3 protein	gb AAF35985.1 AF1	%0L	91	315
143	[Homo sapiens]	78432 1	100%	303	329
522	(AK000265) unnamed	gil7020230 dbj BAA9	41%	545	545
522	protein product [Homo	1041.1	53%	689	594
522	sapiens		0,75	300	190
	 	PF00018	58.42	308	CO+
	domain 3		7007	216	535
blastx.2	-	dbj BAA91041.1	40%	C17	
	protein product [Homo				
,	sapiens		20.64	901	781
909683 144 HMMER	PFAM: Src homology	PF00018	39.04	071	
blastx.2	-	gb AAA16358.1	35%	33 324	527 527
911357 145 HMMER	+-	PF00018	14.09	989	853
	-+	11 4 0 0 0 0 0 1 1	470%	95	874
blastx.2	(AF053130)	gb AAC40124.1	%999	788	898
	unconventional myosin		200		
	+	DE00017	42.63	14	202

			8 -	domain 2				CCC
			blastx.2	24) hypothetical	emb CAB43208.1	%88	7	775
				piens	COA A LA OCCAGEN	81%	99	593
HELHI69	1128924	147	blastx.14		gij4/04/39 gp AAD2	%92	586	624
				containing protein Nsp3	8240.1 AF12421_1	52%	590	640
				[Homo sapiens]		%09	55	66
						63%	612	644
				THE CONTRACTOR	PE00017	72.59	241	483
HELHJ69	911262	524	HMMER	PFAM: Src nomorogy				
	- · - ·		8.1	domain z	OHIA AD28246 11AF1	78%	19	645
			blastx.2	(AF124251) SH2-	24751 1	%9L	587	625
				containing protein inspa	1-10747	%09	99	100
-				Homo sapiens	11000011	46.0	758	1036
HFKLA09	952634	525	HMMER	PFAM: Src homology	Pr00017); }		
			2.1.1		DE00017	69.47	384	614
HSBBF79	965764	149	HMMER		FFUUUI /		-	
			1.8			37.75	301	405
HSLKA77	911589	526	HMMER		PF00017	(2.10		
			1.8	-	abl A A 49087 11	58%	178	432
			blastx.2	tensin [Gailus gailus]	Rollandaria	51%	29	115
			٠			31%	3	155
					211800055tahlA A B4	%69	848	1150
haedr21	1090433	151	blastx.14	p66shc [Homo sapiens]	giltozyczylgopania	72%	134	412
0					17712.1	29%		475
						37%	599	751
				_		35%		164
				-		34%		778
	10001	507	blastx 14	MUS p66 Shc [Mus	gi 1200456 gb AAA9	%16	62	268
nagdr21	100717	1		musculus	\dashv	7006	68	1609
HHENH27	1025277	152	blastx.2	collagen alpha 1(III) chain	pir S05272 CGHU/L	3070		
11111 11110								

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1741	160	174	160	173	174	161	183	173	174	59	65	16	56	45	99	9	25	36	Ś	73	4	7	7	5	2	ιŋ	΄	ব	4	7
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1061	1094	956	1094	851	83(1073	109	1022	1088	7	∞	∞ ∞	_	7	12	∞	2	4	· v	7	m			(7)	(1	(4			. ,	17
30%	32%	32%	32%	31%	30%	30%	28%	28%	30%	30%	30%	34%	28%	27%	32%	30%	34%	30%	28%	34%	28%	35%	33%	28%	36%	78%	30%	27%	30%	79%
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9591	1848	1662	525	525	525	1659	9591	1644	642	534	592	654	226	869	648	229	589	211	226	250	226	190	259	125	128	213		212
																						*						
31%	32%	29%	36%	37%	32%	33%	30%	30%	32%	34%	33%	30%	39%	28%	30%	41%	30%	37%	34%	33%	35%	43%	36%	44%	52%	49%		46%
						-												,								3AA9		BAA9
																										91505[1		161 dbj
																				,						sp BAA91505 BAA9		gi 7022161 dbj BAA9
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			•								ł															43 FIS	31, MLAR	nnamed
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																										CDNA FLJ10243 FIS,	CLONE HEMBB1000631, WEAKLY SIMILAR TO	1 (AK 001105) unnamed
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		61					3	-		122	771		131	 }		CI	71		136	000		15	<u></u>				
	100%	12031	1	v	53%		100%			10 00	70.81		000	30.0		000	19.89		001	109			45%				
1505.1	gi 7022415 dbj BAA9 1590.1	DE00004	Process		gi 2291232 gb AAB6	5351.1	oil1651401ldbilBAA3	5601.1			PF00004	-		PF00004			PF00004			PF00004			emb CAA93516.1		-		
product [Homo	sapiens] (AK001267) unnamed protein product [Homo			associated with various			domain: I elegalis	protease ATP-binding	subunit ClpA.	[Escherichia coli]	PFAM: ATPases	associated with various	cellular activities (AAA)	PFAM: ATPases	associated with various	cellular activities (AAA)	PFAM: ATPases	associated with various	cellular activities (AAA)	PFAM: ATPases	associated with various	cellular activities (AAA)	Similarity to Yeast MSP1	protein (TAT-binding	homolog 4)	(SW:MSP1_YEAST)	[Caenorhabditis elegans]
	blastx.14	 -	HMMER		blastx.14			blastx.14			HMMER	1.8		HMMER	2.1.1	0	HMMER	1.8		HMMER	2.1.1		blastx.2				-
	154	-	529					155			530			156	; i		531	·		158							
	1151374		947872		,			1128800			781946			8270768	070170	_	455474			947881	100/1	-					
	HAPNV33		HAPNV33					HBTAE84			HBTAF84	TOTAL OIL		HNPVV80	UDF v 162		TCT DD21	ן מטבטטבו		LIMITAN37	CNIMINIU						

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	421	778	. 565	799	733	733	751	709	715	2120	2166	932	900	1283	243	700	200		
	224	185	335	095	623	674	626	554	. 506	1164	2104	295		1650	37		61		
	9.79	100%	64%	52%	32%	45%	26%	80.1	21%	080	%08	1 696	1.202	249.7	97.9		42%		
2650.1 AF176012_1	PF00226	gi 5815353 gb AAD5 2650.1 AF176012_1	Gil3881075lemblCAA	21734.1	¥			PF00226	gi 3881075 emb CAA 21734.1	I A A GI:-III-ID A A 1	gi 179980o doj BAA1 6264.1	7331044	Pr01556	PF01556	PF00226		gi 1707079 gb AAB3 7835.1		
-	apiens	heat shock protein. (AF176012) J domain containing protein 1	isoform a [Homo sapiens]	(AL032657) predicted using Genefinder; similar	to 1111ES			PFAM: DnaJ domain	(AL032657) predicted using Genefinder; similar	to 111ES	similar to [SwissProt Accession Number	P08409]; 1	PFAM: DnaJ C terminal region	PFAM: DnaJ C terminal	region nr v M. Daol prokarvotic	PFAINI: Dilas, proxary cus	contains strong similarity to a DNAJ-like domain	(PS:PS00636)	Caenorhabdins elegans
	HMMER	1.8 blastx.14		blastx.14				HMMER	2.1.1 blastx.14		blastx.14		HMMER	HMMER	2.1.1	HMMEK	blastx.14		
	537			165				538		,	166		539	540		541			
	949211			1177932				908840			1106041		596802	929762		818806			
	HAGAX57			HAMGX15			,	HAMGX15			HAUBV06		HAUBV06	HAUBV06		HBWCM62			

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322	274	364	904	229	256	357	269	185	8	421	445	762
89	08	89	71	89	80	37	466	505	248	203	200	99
%86	116.61	%86	%9L	65.68	49%	100%	68.48	100%	100%	78.3	100%	88.67
gi 1651491 dbj BAA3 6142.1	PF00226	gi 1651491 dbj BAA3 6142.1	gi 7022789 dbj BAA9 1724.1	PF00226	gi 1232165 emb CAA	gi S815355 gb AAD5 2651.1 AF176013_1	PF00226	gi 5815355 gb AAD5 2651.1 AF176013_1	gi 402674 gb AAA18 299.1	PF00226	gi 402674 gb AAA18 299.1	PF00226
ed DNA-binding ein cbpA [Escherichia	aryotic	shock protein ed DNA-binding in cbpA [Escherichia	coli] (AK001496) unnamed protein product [Homo	sapiens PFAM: DnaJ, prokaryotic	heat shock protein cysteine string protein	(AF176013) J domain containing protein 1	isotorm b Homo sapiens] PFAM: DnaJ, prokaryotic	(AF176013) J domain containing protein l	ORF-1 [Escherichia coli]	PFAM: DnaJ domain	ORF-1 [Escherichia coli]	PFAM: DnaJ, prokaryotic heat shock protein
blastx.14	MER		blastx.14	HMMER	1.8 blastx.14	blastx.14	HMMER	1.8 blastx.14	blastx.14	HMMER	blastx.14	HMMER 1.8
168	542		169	543		170	544		171	545		546
1105672	908820		1107236	908837		1151469	949210		1148741	935730		98836
HCWFA35	HCWFA35		HDACA35	HDACA35		HDQGM08	HDOGM08	·	HELGB06	HELGB06		HEOPR74

					2:11 22 1 63 Jamph C A 1	41%	80	707
			blastx.14	cysteine string protein	63354.11	20%	457	492
HIBEK35	731480	173	HMMER	PFAM: DnaJ domain	PF00226	112.7	237	404
HJMAR88	908839	547	HMMER	PFAM: DnaJ domain	PF00226	42.7	57	149
		,	2.1.1 blastx.14	cysteine string protein 1 -	pir S70515 S70515	68% 100%	6	254 60
HMWGU56	908825	548	HMMER	PFAM: DnaJ domain	PF00226	126.9	375	569
,			blastx.14	Similarity to B.subtilis	gi 3873707 emb CAA	59%	327	587
				DNAJ protein i [Caenorhabditis elegans]	1.01+16	34%	51	200
HOUDS09	1164010	176	blastx.14	(AK000034) unnamed protein product [Homo	gi 7019854 dbj BAA9 0896.1	35%	240 729	059
				sapiens]		45% 32%	96 174	248
HOUDS09	949051	549	HMMER 1.8	PFAM: DnaJ, prokaryotic	PF00226	98.53	310	504
			blastx.2	(AK000034) unnamed protein product [Homo	dbj BAA90896.1	53%	37 899	1033
				sapiens		63%	7 03	197
HTEGM38	180519	177	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	7.00	6	171
HTEKY82	908846	550	HMMER	PFAM: DnaJ domain	PF00226	119.6	781	C/4
			blastx.14	Similarity to B.subtilis DNAJ protein 1	gi 3873707 emb CAA 97416.1	23%	236	502
HTLCY54	1193550	179	blastx.14	MDJ6.	sp Q9QY17 Q9QY17	94%	239	460 927

			,																						_				٦.
597	669	445	919	934	694	169	401	-		708		896	007		516		318		363	413	364	-	175	100	700	167	700	420 804	
484	019	245	239	797	632	611	183			124		-			130	132	10	2	10	346	320	076	-	.		- 017	412	504	70/0
81%	73%	119.8	%19	78%	47%	40%	137.85			386.54			108.8		. 043	04.9	105 05	05.601	%88	0.700	0//0	100%		83.68		%89	26%	90%	3770
		PF00226	oil3402485ldbilBAA3	2009 11			PF00211			PF00211			PF00211			PF00069		PF00069	CA A CHEROLOGIA	gi 3241849 ab bAA2	8870.1			PF00069	-	gi 5052670 gb AAD3	8665.1 AF145690_1		
-		PFAM: DnaJ domain	A DOLAGOO MR I CHOMO		sapiens]		+	FFAINI, Aucilylaic and	Guaily inc cycings	PFAM: Adenylate and	Guanylate cyclase	catalytic domain	te and	Guanylate cyclase	catalytic domain	PFAM: Eukaryotic protein	kinase domain	PFAM: Eukaryotic protein	KIDASE GOIDANI	calmodulin-dependent	protein kinase II-delta	dash [Oryctolagus	cuniculus]	PFAM: Eukaryotic protein	kinase domain	(AF145690)	BcDNA.LD28657	[Drosophila melanogaster]	
		HMMER	2.1.1	blastx.14			10 O U.	HMMEK	0.1	HMMER	1.8		HMMER	2.1.1		HMMER	2.1.1	HMMER	1.8	blastx.14				HMMER	8	blastx.14			
		551					0	180		181		۲	182			183		184						185					
		908832						603245		837703			857884			732597		91:1312		-				921782					
	-	HTLCY54			7		,	HFOXK14		писводо	1111111 000		HHFI 1106			HAGBA56		HAGGF84				·		HAHGD33	CCADINII				

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			0.00		PE00069	74.92	39	8/7
HAHIY08	962113	186	HMMEK	your process				
			1.8	Kinase domain	CAOA ALTERACORON	4/10/	192	278
			blastx.14		gi 4/0364 gb AAC4/	0/44	3/1	60
				[Caenorhabditis elegans]	047.1	58%	108	179
						101	5	365
HBIOZ10	973131	187	HMMER	PFAM: Eukaryotic protein	PF00069	1.121	7	
			1.8	kinase domain	11 001750 111	7009	c	305
			blastx.2	(AF003134) strong	gb[AAB54159.1]	7/00)	
				similarity to the				
	_			CDC2/CDX subfamily of			1	
				ser/thr protein kinases				
				[Caenorhabditis elegans]		000		213
HRKDI30	729048	188	HMMER	PFAM: Eukaryotic protein	PF00069	42.23	→	C17
a Circuit	1		1.8	kinase domain			000	ECV
HBXBW40	706115	189	HMMER	PFAM: Eukaryotic protein	PF00069	34.01	087	C74
			1.8			30.70	010	347
HCEHE35	909937	190	HMMER		PF00069	30.70		
			1.8		1	7077	700	398
			blastx.14		gi 914100 gb AAB33	0,00	704	COC .
	·.			[human, DX3 B-cell-	346.1			
				myeloma cell line,				
				Peptide, 984 aa] [Homo				
			-	sapiens]		03 60	c	096
HCFPW85	911374	161	HMMER	PFAM: Eukaryotic protein	PF00069	83.32	·	201
			1.8	kinase domain		/010	1	096
			blastx.14	predicted using	gi 3875903 emb CAA	0/./8	^	2024
				Genefinder; Similarity to	94127.1			·
				1 1 1 cDNA		770	751	231
HCFAT25	932068	192	HMMER		PF00069	0.02	00.	
•			2.1.1	-	10 A A L 1 D CO COC	7029	91	456
			blastx.14	(AF096300) HPK/GCK-	gi 4322936 gb AAD1	0270		
					,			

951 09		518 509			15 92	20 295	11 145		68 433	737/	+C/ C) / C	709	331	11,50	0511 150			740	720	978		760 220		3 302	170	192 458
72%	0/07	26%	11%	42%	61%	89.54	41.11	41.11	98.74	0,000	706.65	7000	92%	0. 00	87.19		95%	89%		73.4	7000	18%0	4470	92.5		93.6	, 600	35%
6137.1		gi 2088685 gb AAB5	4139.1			PF00069	0,000	PF00069	PF00069		PF00069		gi 2304746 emb CAA	03387.1	PF00069		dbj BAA85045.1		*	PF00787		gi 294637 gb AAA42	137.1	PF00069		PF00069		gi 1517820 gb AAC5 0918 11
ase HGK [Homo	sapiens	(AF003134) strong	similarity to the	CDC2/CDX 1		yotic protein	-	votic protein	FFAM: Fukaryotic protein	-	PFAM: Eukaryotic protein	kinase domain	HUMAN NDR	[unidentified]	PFAM: Eukaryotic protein	kinase domain	(AB026289) protein	kinase SID6-1512 [Homo	sapiens	PFAM: PX domain		serine/threonine protein	kinase [Rattus norvegicus]	PFAM: Eukaryotic protein	kinase domain	PFAM: Eukaryotic protein	kinase domain	p56 KKIAMRE protein
		blastx.14 (HMMER					├	1.8	blastx.14		HMMER	1.8	blastx.2			HMMER	2.1.1	blastx.14		HMMER	2.1.1	HMMER	2.1.1	blastx.14
<u></u>		193				552		194	105		961				197					861				553		200		
		1139731				894415		810305	100010	470010	934520	,			999696					919027			,	895106		934472		
		HCFCF47				HCFCF47		HDAAV61	2 COMMON	HDFND/3	HDPNC96		-77		HDPSR15					HDODX20	, 			HDOHB19		HDTBY88		

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HE2KZ07 909948 201 HE8UY74 960914 202 HE9NO66 974353 203		HMMER					
909948				DE00069	115.19	5	789
960914		_	PFAM: Eukaryouc proteim kinase domain	7000011			
960914	_ 	-		gi 3135197 dbj BAA2	%96	17	433
960914			dulin-	8263.1	26%	418	700
960914			dependent protein kinase I				
960914		-	beta 2 [Rattus norvegicus]		000	711	407
974353		HMMER	PFAM: Eukaryotic protein	PF00069	36.37		407
974353	<u>.</u>	1.8	untaine	oil3600036lgblAAC3	36%	1117	290
974353	_	Diasix.14		5524.11	45%	13	Ξ
974353				-	73%	366	410
974353	-		NIIIdaac 1		37%	467	553
	03	HMMER	PFAM: Eukaryotic protein	PF00069	121.6	473	757
	1	~	kinase domain				
		blastx.14	(AB020741) NIK-related	gil6009519ldbj BAA8	73%	449	817
			kinase (Mus musculus)	4943.11	94%	2	782
			Ferrosanii carril ocurru	-	79%	748	066
HFMRT61 939957 20	204	HMMER	PFAM: Eukaryotic protein	PF00069	9.92	91	285
		2.1.1	kinase domain		-	,	441
		blastx.2	(AD000092) hypothetical	gb[AAB51171.1]	71%	13	441
			human serine-threonine	• .		· · · ·	
			protein kinase R31240_1				
			[Homo sapiens]				416
HETLF29 909762 20	205	HMMER	PFAM: Eukaryotic protein	PF00069	143.18	9	410
		1.8	kinase domain				711/
		blastx.14	similar to cAMP-	gij3878636 emb CAA	26%	0	410
			dependant protein kinase;	88953.1			
			cDNA EST 1 1 1			C	177
HFIUE75 909758 20	206	HMMER	PFAM: Eukaryotic protein	PF00069	89.68	3//	+000
		1.8	kinase domain				

634	715	774	270	0	270	110	90	866	100	161	000	803	563	1	4/4	į	4/1			11//	076	80/	408		17.1	17771	+/71	1352	
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43%	46%	47%	34.65		21%	40%		200.01		58.81		19%	70%		83.4		%06			89.46	- 30	39%	33%		31.4		69.4	%68	
gi 1905906 gb AAB5	1171.11	-	PF00069		pir A38282 A38282			PF00069		PF00069		gi 5052670 gb AAD3	8665.1 AF145690_1		PF00069		dbj BAA85154.1			PF00069		gi 2262107 gb AAB6	3615.1	-	PF00069		PF00566	gb AAF28980.1 AF1	
(AD000092) hypothetical		,	otic protein	kinase domain	p58 galactosyltransferase-	associated protein kinase -	human	PFAM: Eukaryotic protein	kinase domain	PFAM: Eukaryotic protein	kinase domain	(AF145690)	BcDNA.LD28657	[Drosophila melanogaster]	PFAM: Eukaryotic protein	kinase domain	(AB016589) inducible	IKappaB kinase {Mus	musculus	PFAM: Eukaryotic protein	kinase domain	(AC002343) Ser/Thr	protein kinase isolog	[Arabidopsis thaliana]	PFAM: Eukaryotic protein	kinase domain	PFAM: TBC domain	(AF161420) HSPC302	7
blastx 14			 HMMER	8.	blastx.14			HMMER	1.8	HMMER	1.8	blastx.14			HMMER	1.8	blastx.2			HMMER	1.8	blastx.14			HMMER	2.1.1	HMMER	2.1.1 blastx 2	Ulumini.
			207					208		209					210		,			211					212		213		
			934019			8	-	894409		921783				4	944057					959140					918685	÷	919354		
			HFKIT06					HHEGG20		HHEHC53					HHERO79					HISAF59					HKAKM10		HLTHP86	 	

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%66	52%	26.49	21.34	102.96		55%	130.82		52%	33%	57%	22%	94.55		96.28	%26	85%	74%	77%	%69	989	%09	52%	37%	39%	35%	33%
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	[FIOURO Sapiens]	PFAM: Eukaryotic protein	PFAM: Eukaryotic protein	Kınase domain PFAM: Eukaryotic protein	kinase domain	(AC006530) unknown [Homo saniens]	PFAM: Eukaryotic protein	kinase domain	LATS (Drosophila	melanogaster	T	-	PFAM: Eukaryotic protein	kinase domain	PFAM: Eukaryotic protein	Kinase dolliani	calmoduliii-biiidiig	protessionel	lioi vegicus]								
		HMMER	HMMER	1.8 HMMER	8.1	blastx.14	HMMER	1.8	blastx.14				HMMER	8.	HMMER	1.8	blastx.14						1				
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538	657	370	493	921	915.	423	384	+00	183	Op F	103	674	100	+71	00,7	404				710	246	340	040	425	889		248	323	750
512	556	86	131	763	751	211	157	/С1	107	171	110	1117	-		,	7				406		1/	388	342	662	,	33	33	CC
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		yotic protein	KIIIase uoinami	mixed-lineage protein	Kinase 1 - numan	PFAM: Eukaryotic protein	kinase domain	yotic protein	kinase domain	similar to protein kinase	of X.laevis, has putative J	PFAM: Eukaryotic protein	kinase domain	PFAM: Eukaryotic protein	kinase domain	(AJ271722) putative	serine/threonine protein	kinase MAK-V [Homo	sapiens	PFAM: Eukaryotic protein	kinase domain	(AB023658)	Ca/calmodulin-dependent	protein kinase kinase	alpha, CaM-kinase kinase	alpha [Rattus norvegicus]	PFAM: Eukaryotic protein	kinase domain	kinase like protein
		HMMER	1.8	blastx.14	_	HMMER	1.8	HMMER	8.1	blastx.2		HMMER	1.8	HMMER	1.8	blastx.2				HMMER	8.1	blastx.2			.,,		HMMER	2.1.1	blastx.2
		220				554		222				223		224						225							226		
_		974911				911566		945856		-		888037		717358						942527							942673		
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303	122	95		601	,			ε.		m ;	489	892	1023	428		722	1070	428	613		604	209	61	.			579	/83
20%	79.36	53.16		27.09		85%	-	50.8		85%	64%	85%	38%	200.58		41%	36%	29%	114.85		46%	29%	99.16		44%		55%	44%
	PF00069	PE00069		PF00069	-	gi 3715669 emb CAA	03585.1	PF00069		gi 205278 gb AAA41	562.1	-		PF00069		gb AAD32787.1 AC0	07661 24		PF00069	-	gb AAB03535.1		PF00069		gi 406113 gb AAA19	670.1	gi 495684 gb AAA50	735.1
[Arabidopsis thaliana]	otic protein	Kinase domain		votic protein	kinase domain	CYCLIN-DEPENDENT	KINASE (CDK)8	PFAM: Eukaryotic protein	kinase domain	male germ cell-associated	-	_	[choigo Holl	PFAM: Eukaryotic protein	kinase domain	(AC007661) putative	protein kinase	[Arabidopsis thaliana]	PFAM: Eukaryotic protein	kinase domain	MEK Kinase 3 [Mus	musculus	PFAM: Eukaryotic protein	kinase domain	protein kinase I [Rattus	norvegicus	contains EGF-like repeats;	highly similar to ZC84.1;
	HMMER	1.8	HMIMIEK 18	HMMER	1.8	blastx.14		HMMER	2.1.1	blastx.14				HMMER	1.8	blastx.2			HMMER	1.8	blastx.2		HMMER	1.8	blastx.14		blastx.14	
	227	000	877	229		-		230	5					231	,	, -			232	1			233				234	
	823869	1	911294	921593				037583	175707					953308					044410				909843				1151075	
-	HSKAC24		HSSMT34	HT3BG12				11775006	niedow					HTEKT33					UTENIIKE	111			HTEMV09				HTFMV66	

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772	315	926	571	730	373	179	220	116		223	C	890	207	307	030	757	972	414	579	621	933	700	930	1100	1150	1190		
198	154	755	371	641	323	315	100	324		44		35	0,00	437	267	//0 -	640	142	427	595	166	00,	155	000	0701	054	100	
23%	27.8	%05	38%	%09	52%	31.25		45%		0.55	55.9	/00/	09%	40%	42%	38%	46%	48%	45%	42%	251.19		44%		32.41	720/	1370	
	PF00069	11106100120171	gl/100102 cm 76028 11	1.0200	-	PF00069		emb CAB76028.1			PF00069		gi 4868443 gb AAD3	1319.1 AF144573_1			sp 061241 Q61241				PF00069		gb[AAA99535.1]		PF00069	DO 4 41 1 100 4 00 1 100	gi 34524/3 gb AAC/ 1014.1	
-	yotic protein	kinase domain	(AL157917) similarity to	endopeptidases 1		PFAM: Eukaryotic protein	kinase domain	(AL157917) similarity to	endopeptidases	Schizosaccharomyces 1	PFAM: Eukaryotic protein	kinase domain	(AF144573) Mx-	interacting protein kinase	PKM [Mesocricetus	anratus	TESTIS-SPECIFIC	CEDINE/THREONINE	SEMINE/ HINCOMINE	NIMASE.	PFAM: Eukaryotic protein	kinase domain	serine/threonine kinase	[Mus musculus]		-	(AF084205)	kinase TAO1 [Rattus
	MER	2.1.1	blastx.14		-	HMMER	1.8	blastx.2			HMMER	2.1,1	blastx.14				blocty 14	Ulasta. 17			HMMER	8.	blastx.2		HMMER	1.8	blastx.14	
	555		235		,	556		, ·			236						227	/ 57			557				238			
	813038		1175071		-	940369					973302						1070101	1718091			942161				008996.			
	HTEMV66		HTGAU79		,	HTGAI179) O I I				HTLEJII							HILIY52			HTI IV52				HTOAK34			

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250	333	353	622	58	759	494	910	344	21.	20	53	243	218	215	467	21	338	243	6	104		859	1296	1404	1742	439	18
E	7/	6	350	2	439	345	611	267	123	57	3	211	162	6	988	123	267	211	45	3		425	1159	1282	1695	182	10
	114.02	94%	95%	63%	34%	48%	34%	57%	48%	24%	47%	72%	42%	34.73	150%	45%	37%	54%	41%	27.74		%65	41%	39%	75%	31.12	84%
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norvegicus]	PFAM: Eukaryotic protein kinase domain	(AT 117482) hynothetical	(11111) (110m) formand	protein [rioino sapiens]	serine/threonine kinase	Pattus norvegions						•		PFAM: Eukaryotic protein	Niliase dollianii	AMP-activated protein	kinase nomolog [riomo	sapiensj		PFAM: Fukarvotic protein	kinase domain	PRO1038.)			PFAM: Eukaryotic protein	(AF191838) TANK
	HMMER	Floety 7	Diasta.2	•	blooty 14	Ulasta.14	- 10							HMMER 1.º	1.0	blastx.14				HMMFR	1 8	hlastx 14				HMMER 1.0	blastx.14
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	HTPGG25		-			HOJAD24					-			HUJAD24						111707111	HUISFII	111WC700	007D \ AH			HUVGZ88	HWADY66



			Homo sapiens		0000		177
	999	HMMER 18	PFAM: Eukaryotic protein kinase domain	PF00069	78.87		+/1
952878	244	HMMER	PFAM: Eukaryotic protein	PF00069	93.74	1655	945
		0.1	A COOSTAST CONTRACT	wil2262107loblAAB6	41%	1655	1383
		blastx.14	(AC002343) 351/1111	3615 11	48%	1319	1185
			protein amase isolog		42%	1046	933
			[Alabidopsis manama]		75%	1355	1332
948434	245	HMMER	PFAM: Eukaryotic protein	PF00069	115.98	225	632
,		1.0 Floats 14	(AE15684) RIP-like	oi15059425leblAAD3	91%	165	632
		Ulasta. 14	kinase [Homo saniens]	9005.11AF156884 1	%99	702	773
				-	100%	632	199
1150212	246	blastx.14	(AF156884) RIP-like	gi 5059425 gb AAD3	82%	-	273
	-0.	rn o trn	Kiliase [Hollio sapicils]	PE00069	64.17	4	273
894404	261	HMIMEK 18	Fraivi. Eukarjouic protein kinase domain				
927676	247	HMMER	PFAM: Eukaryotic protein	PF00069	32.82	190	381
		1.8	kinase domain				000
		blastx.2	(AF169034) protein	gb AAF12757.2 AF1	965:	154	476
			kinase [Homo sapiens]	69034_1	100%	69	100
				-	2170	707	
934505	248	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	147.2	2	916
•		blastx 2	(AC005581) R31237 1,	gb AAC33487.1	%06	89	364
			partial CDS [Homo		100%	2	9/
			sapiens		40%	306	422
955336	249	HMMER	PFAM: Eukaryotic protein	PF00069	122.85	1458	934
		1.8 hlastx 2	(AK000528) unnamed	db BAA91232.1	100%	3	572

		604	10/		7:1	610		505	770	766	200	66,	432	3	732		059	0	728		283	1012	1321	596		374	2 6	C47	350	
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		57%	0/			81.59		-	100%	,	123.84		86		92		206.82		6		92	3(56	4		6		01	6	
	"	22			1			-	A3				AA3		.D2	-	<u> </u>		ND2		D2		<u> </u>			1D2	-		AA7	
		gb AAA							2 db] B.⁄)2 dbj B/		11 gb AA	F062595			11 gb AA	F062595	41leblA	F062594	1 00427.			41 gb A	F06259	· .	00 db B	
	_	gi 144039 gb AAA22	969.1			PF00196			gi 1651302 db BAA3	5352.1	PF00072		gi 1651302 dbj BAA3	5352.1	gi 4691541 gb AAD2	7956.1 AF062595_1	PF00406		gi 4691541 gb AAD2	7956.1 AF062595_1	oi146915411gblAAD2	7056 11 A F067595	eli occi	PF00406		gi 4691541 gb AAD2	7956.1 AF062595	PF00406	gi 4760600 db BAA7	0
-				etella			ıxR			,							-				T			inase		ite	ens	inase	ate	
protein product [Homo	<u>.</u> .	e le	transcription regulator	(put.); putative [Bordetella		erial	regulatory proteins, luxR		Regulatory protein KdpD	coli	onse	regulator receiver domain	Regulatory protein KdpD	colil	(AF062595) adenylate	kinase 5 [Homo sapiens]	PFAM: Adenylate kinases	•	(A F062595) adenylate	kinase 5 [Homo sapiens]	(AE062505) adenylate	auciiy ia	Kinase 5 [Homo sapiciis]	PFAM. Adenylate kinase		(AF062595) adenylate	kinase 5 [Homo sapiens]	PFAM: Adenylate kinase	(AB020203) adenylate	man
in produ	ns]	BygA positive	cription); putativ	ssis]	PFAM: Bacterial	atory pr	ly	latory p	Escherichia coli	PFAM: Response	lator rec	ılatory p	Escherichia coli]	062595)	se 5 [Ho	M: Ade		(565690	se 5 IHo	(\$0\$05)	(5,5500	se o l'uo	M. Ade		062595)	ise 5 [Ho	M: Ade	2020203	202020
nrote	saniens	BvgA	transe	(put.)	pertussis	PFAI	regul	family	Regu	[Escl	PFA	regu	Regu	[Esc]	(AF	kina.	PFA		/A F	kina	WILLIAM (A E)	ر ا ا	Kina -	+-		+-	kina	 -	\top	┪
		blastx.14				HMMER	1.8		blastx.14		HMMER	1.8	blastx.14		blastx 14	orașe de la constant	HMMER	~	Placty 14	Ulasta. 14	11.4.11	Diasix.14		HMMER	111VIIVILIA 2-1-1	2.1.1 blastx.14		HMMER	2.1.1 blocty 14	Diasta. 14
<u> </u>		250)	,		562			251		563		.		252	2 67	564	-			0.00	507		375	COC -			254		
		1105673				974478			1103374		953059				1150845	C+000	057992	7(()	•		0.00	1149319		2002	566166			934887		-
		10	-			974.	<u> </u>		110		953				1=		057				-	711						93,		-
		HCWDV17				HCWDV17	:		HELDI95		HELD195				A OTO 36	HAGF023	UAGEODS	HAULO25				HAWAB54	,	A D CL A TAY A YA	HAWAB34			HLIBV06	•	
		Ξ	1			Į	:			<u> </u>	1				Ţ							<u>Г</u>								

			,	zyme 3 [Mus	7360.1			
HMALL66	1105097	255	blastx.14	adenylate kinase (EC 2.7.4.3), chloroplast -	pir S45634 S45634	45%	. 71	292
HMALL66	956195	999	HMMER	marze PFAM: Adenylate kinases	PF00406	50.17	63	296
HOACE12	858976	256	1.8 HMMER	PFAM: Adenylate kinase	PF00406	46.1	20	235
699ЭЭОН	924848	257	2.1.1 HMMER	PFAM: Adenylate kinases	PF00406	76.14	858	1145
			blastx.14	adenylate kinase (EC 2 7 4 3) chloroplast -	pir S45634 S45634	36%	480 849	1145
				maize		33% 57%	3/9	255
HAGAE09	525926	567	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding	PF00130	3.93	159	185
HAGAE34	525878	568	HMMER 1.8	dollialli PFAM: Phorbol esters / diacylglycerol binding	PF00130	8.88	191	253
HARMH78	1137572	260	blastx.14	domain (AF001435) unknown [Homo sapiens]	gi 2529709 gb AAB8 1205.1	32% 43% 75%	237 135 482	395 203 505
HARMH78	773210	695	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding	PF00130	4.88	192	227
HBJLB53	974122	570	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding	PF00130	4.62	301	348
HRINB52	726475	571	HMMER	PFAM: Phorbol esters /	PF00130	3.77	193	7C7

	284	393	867 1230 1662	546	651 806	356	89.	- (109	437
	255	253	286 1018 1537	415	654	333	21	288	74	387
	6.04	25.6	54% 46% 23%	26.42	94%	2.94	5.7	%86	4.09	2.97
	PF00130	PF00130	sp O15463 O15463	PF00130	gi 1504026 dbj BAA1 3212.1	PF00130	PF00130	gi 1702880 emb CAA 70746.1	PF00130	PF00130
diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PTPL1-ASSOCIATED RHOGAP.	PFAM: Phorbol esters / diacylglycerol binding domain	similar to C.elegans protein (Z37093) [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	mhpR [Escherichia coli]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain
1.8	HMMER 1.8	HMMER 1.8	blastx.14	HMMER 1.8	blastx.14	HMMER 1.8	HMMER 1.8	blastx.14	HMMER 1.8	HMMER 1.8
	572	573	265	574		575	576	268	577	578
	669619	616980	1212494	970586		952734	913787	1121872	867276	947947
	HDABQ83	HDPDC84	HDPUF40	HDPUF40	·	HDPWU07	HDTJJ02	HE2GA18	HE2GA18	HE2SY03

The state of the s

301	390		206	348	375	236	156	395	22 213 274	90
456	241	29	147	322		292	115	354	165 266 342	. 64
46%	76.38	3.29	7.32	3.23	100%	6.2	1.4	10.16	37% 55% 39%	3.27
gi 4836401 gb AAD3 0425.1 AF118023_1	PF00130	PF00130	PF00130	PF00130	gi 7020117 dbj BAA9 1000.1	PF00130	PF00130	PF00130	gi 182221 gb AAA58 464.1	PF00130
(AF118023) SH3 domain- binding protein SNP70 [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / . diacylglycerol binding domain	(AK000193) unnamed protein product [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	ORF 3 [Homo sapiens]	PFAM: Phorbol esters / diacylglycerol binding
blastx.14	HMMER 1.8	HMMER 1.8	HMMER 1.8	HMMER 1.8	blastx.14	HMMER 1.8	HMMER 1.8	HMMER 1.8	blastx.14	HMMER 1.8
	579	580	581	582	274	583	584	585	277	586
	934511	697730	960741	771320	1151481	791469	923895	966924	1107392	871911
	HELGY64	HFIYW31	HFVIP88	HGBAS76	ННЕВВ62	нневв62	ннени73	HHEMAII	ннеоко1	ННЕОКОІ

where the control were were the control was the control with the control was the control with the control was the control was the control were the control was

	187	364	206	1257	1437	891	756	1650	158	233	137		378	183	652 871 127
	146	2	177	904	1279	754	902	1627	102	207	84		328	136	275 719 32
	12.35	276.4	3.12	28% 88%	54%	43%	47%	87%	42%	5.32	3.59		4.83	3.46	59% 52% 37%
	PF00130	PF01800	PF00130	sp Q9VGN8 Q9VGN 8						PF00130	PF00130	•	PF00130	PF00130	gi 1504026 dbj BAA1 3212.1
domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Sterol O- acyltransferase	PFAM: Phorbol esters / diacylglycerol binding domain	CG5276 PROTEIN.				20	,	PFAM: Phorbol esters / diacylglycerol binding	PFAM: Phorbol esters /	diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	similar to C.elegans protein (Z37093) [Homo sapiens]
	HMMER 1.8	HMMER 2.1.1	HMMER 1.8	blastx.14		•				HMMER 1.8	HMMER	1.8	HMMER 1.8	HMMER 1.8	blastx.14
	278	587	588	281						290	591		592	284	285
	915639	706739	504326	1220254						619896	464241	1	626559	662405	1151494
	HHPEM84	HHSED84	HIBCC94	HKADN56						HKADN56	HKIXG58		HLICI13	HLTGF17	HLYDC50

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319	803	175	3 35	8 . 226	6 152	3 146			0 632	0 213
161	2212	131		158	126	123	175		009	190
29.67	100%	3.79	3.04	6.77	3.33	3.13	3.15	3.9	5.19	3.1
PF00130	pir E65035 OXECLD	PF00130	PF00130							
PFAM: Phorbol esters / diacylglycerol binding domain	L-aspartate oxidase (EC 1.4.3.16) nadB [validated]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Phorbol esters /
HMMER 1.8	blastx.14	HMMER 1.8	HMMER							
593	286	594	595	969	297	598	599	009	601	602
677050	1217031	867481	792383	681745	778884	859932	958329	740087	922022	531061
HLYDC50	HMADD49	HMADD49	HMEKE78	HMSHU26	HNEEB82	HNHIA06	HODFY16	HPQSB68	HRDBH04	HSICR69

man, the control was some the control of the contro

			domain				
793624	603	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding	PF00130	3.15	207	239
1104299	296	blastx.14	935) mytonic hy kinase-related binding kinase	gi 2736151 gb AAC0 2941.1	94%		931
660053	604	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	22.31	2	70
855660	297	HMMER 2.1.1	PFAM: Phorbol esters/diacylglycerol binding domain (C1	PF00130	42.4	1660	1803
685425	909	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	7.26	398	433
972982	909	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.17	905	653
		blastx.2	phosphorylation regulatory protein HP-10 - human	pir A61382 A61382	99% 100% 74% 100%	214 1080 827 67	909 1259 1078 213
530316	209	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	5.45	102	125
527144	809	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.53	233	1 07
1152491	302	blastx.14	F10B5.8 [Caenorhabditis	gi 5824432 emb CAB	/4%	32	/00

1144	470		777	437	124	1330			203			391			963	260			124		100		377	00/		292		531
623	420		117	111	2	1289			123			359			715	3			59		41		108	476		230		196
20%	3.36		/000	13%	73%	4.25			10.67			4.03			97.4	52%			9.43		8.96		%96	100%		8.27		33
54223.1	PF00130	,	G V O 1 1 1000 1 1000 1	gi 5824432 emb CAB	54223.1	PF00130			PF00130	-		PF00130			PF00620	gi 7020190 dbj BAA9	1027.1		PF00027		PF00027		gi 6691957 emb CAB	65791.1		PF00027		PF00169
elegans	PFAM: Phorbol esters/	diacylglycerol binding	UUIIIIIII	F10B5.8 [Caenorhabditis	elegans	PFAM: Phorbol esters/	diacylglycerol binding	domain	PFAM: Phorbol esters/	diacylglycerol binding	domain	PFAM: Phorbol esters /	diacylglycerol binding	domain	PFAM: RhoGAP domain	(AK000239) unnamed	protein product [Homo	sapiens	PFAM: Cyclic nucleotide-	binding domain	PFAM: Cyclic nucleotide-	binding domain	(AL109657) dJ842G6.1	(novel protein) [Homo	sapiens]	PFAM: Cyclic nucleotide-	binding domain	PFAM: PH domain
	HMMER	1.8		blastx.14		HMMER	1.8		HMMER	8.1		HMMER	1.8		HMMER 2.1.1	blastx.14			HMMER	1.8	HMMER	1.8	blastx.14			HMMER	1.8	HMMER 2.1.1
	609		J.			610			304			611			612	307			613		614		309		-	615		310
	951114					931037			911621			914556			894607	1165331		,	573794		923800		1141737		,	553382		522953
	HTTDH46					HTT1005			HWHGY45			HWLOR48	,		HWLQX76	HATDD09			HATDD09		HBJGT03		HMTMF45			HMTMF45		HHPDV86

248	699	956	999	995	200	268		430	568	259	151	201	519	849	941	1082	307	
138	433	421 264	399	399	000	161		161	386	107	14	145	40	31	855	1062	47	
46.1	62.3	32% 48%	45.6	75%	10/0	104.77		38%	34%	30.1	82%	63%	176.8	%06	79%	100%	43.25	
PF00071	PF00025	gi 4929218 gb AAD3 3908.1 AF143680_1	PF00025	gi 3687625 gb AAC6	7124.1	PF00025		gi 727191 gb AAA64	266.1	PF00169	gi 3599940 gb AAC3	5430.1	PF00621	gi 3599942 gb AAC3	5431.1		PF00071	
PFAM: Ras family	PFAM: ADP-ribosylation factor family	(AF143680) arf-like protein 2 [Mus musculus]	PFAM: ADP-ribosylation factor family	(AF031903) ADP-	ribosylation-like lactor homolog ARL6 [Mus musculus]	PFAM: ADP-ribosylation.	factors (Arf family) (contains ATP/GTP binding P-loop)	ADP-ribosylation factor	[Candida albicans]	PFAM: PH domain	(AF017368) faciogenital	dysplasia protein 2 [Mus	PFAM: RhoGEF domain	(AF017369) faciogenital	dysplasia protein 3 [Mus	musculus	PFAM: Ras family	(contains ATP/GTP binding P-loop)
HMMER 2.1.1	HMMER 2.1.1	blastx.14	HMMER 2.1.1	blastx.14	•	HMMER	8.	blastx.14		HMMER 2.1.1	bľastx.14		HMMER 2.1.1	blastx.14			HMMER	1.8
311	312		313			314	·	-	-	315			316				317	
732602	907613		907614			907620				909745			909755				912608	
HE8BT56	90НОГОН		HOEJG61	·	XII	HE8PN24				HGBHI37		,	нснок82				HFPCH24	

			blacty 14	ran2h gene product (AA	oil35863lemblCAA37	41%	35	229
				1-183) [Homo saniens]	178 11	40%	337	441
					-	35%	266	325
						53%	443	487
HTTKF86	912689	318	HMMER 2.1.1	PFAM: Ras family	PF00071	29.6	86	223
HCESÁ79	912709	319	HMMER 2.1.1	PFAM: Ras family	PF00071	45.1	19	243
			blastx.14	(AB027137) RAB-26 [Homo sapiens]	gi 5931612 dbj BAA8 4707.1	92%	52	246
HDTBJ28	912714	320	HMMER 2.1.1	PFAM: Ras family	PF00071	28.1	21	137
			blastx.14	Rab12 protein [Canis . familiaris]	gi 437985 emb CAA8 0471.1	%88	21	86
HDPBF48	912783	321	HMMER 2.1.1	PFAM: Ras family	PF00071	26.1	. 33	. 101
			blastx.14	(AL117204) predicted	gi 5832782 emb CAB	48%	123	209
				using Genefinder	55120.1	55%	258	338
				[Caenorhabditis elegans]		%89	33	68
	-				٠.	53%	429	467
HTPFY55	912928	322	HMMER 2.1.1	PFAM: Ras family	PF00071	27.2	240	386
			blastx.14	similar to the RAS gene	gi 1572819 gb AAB0	48%	117	383
				family [Caenorhabditis elegans]	9163.1	%09	396	524
HMSCM47	923632	323	HMMER	PFAM: ATPases	PF00004	121.1	59	652
			2.1.1	associated with various cellular activities (AAA)				
			blastx.2	(AF033862) Lon protease [Arabidopsis thaliana]	gb AAC05085.1	9859	5	. 673
HEOQA56	925132	324	HMMER	PFAM: Ras family	PF00071	62.8	53	154
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	202	438	415	415	399	447	1200	846	636	85	299	256	457	308	369
	23	217	8	323	. 61	46	865	622	580	213	9	2	242	12	124
-	76%	31	59.7	100%	47.2	58%	62%	41%	36%	30.6	49.5	137.4	28.1	170.7	29.3
	gi 213115 gb AAA49 230.1	PF00169	PF00493	gi 5834569 emb CAB 55276.1	PF00004	91181658619b1AAC5	0011.1			PF00071	PF01694	PF00873	PF00595	PF01153	PF00595
(contains ATP/GTP binding P-loop)	GTP-binding protein [Discopyge ommata]	PFAM: PH domain	PFAM: MCM2/3/5 family	(AL035461) dJ967N21.5 (novel MCM2/3/5 family member) [Homo sapiens]	PFAM: ATPases associated with various	LON1 protease [Zea	mays]			PFAM: Ras family	PFAM: Rhomboid family	PFAM: AcrB/AcrD/AcrF family	PFAM: PDZ domain (Also known as DHR or GLGF).	PFAM: Glypican	PFAM: PDZ domain
1.8	blastx.14	HMMER 2.1.1	HMMER . 2.1.1	blastx.14	HMMER 2.1.1	blastx 14				HMMER 2.1.1	HMMER 2.1.1	HMMER 2.1.1	HMMER 2.1.1	HMMER 2.1.1	HMMER
		325	326		327					328	329	330	331	332	333
		925349	929481		969536	*				581528	489201	506604	522826	670041	699379
-		НТРСQ24	HWAE137		HDPSF03					HLHST63	HFAAJ44	HSLEM44	HETCL79	HFTAR20	HCUFD32